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FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTAGAAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTGTTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCTTTCCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGATGCTGGTCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAAAA

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FIGURE 340

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRRE
GKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHITLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL**Important features of the protein:****Signal peptide:**

amino acids 1-28

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FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCGCTACCACCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAACCTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 342

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

Important features of the protein:**Transmembrane domain:**

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

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FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTTTCATAGGCG
ATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTT
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT
GTAA

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FIGURE 344

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
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Signal peptide:
amino acids 1-15

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FIGURE 345

[illegible]

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FIGURE 346

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61; NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVKVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKVRPEEKQQ
AKPVKVERTRKRESEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

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FIGURE 347

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTCCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCTACTCATGACCACCACTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATTGG
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
AGGAGGACAACGCAGCCTGATAAAACAGTGGACGACTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGGAACAGACATTGGAACCTGCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCAATCATCTTGAACATGGAATTTGCTCTGAAGCA
GCAACAATTTGTACATTGGTTCCCGAGATGGATTAGTTTCAAGCTCTCCTTGACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTCTGGGACATCGAAGACAG
CATTAGTCATGAACCTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAAGCCGCA
TGAAAGAATCATCAAACCGGAATATGGGCTACTGATTGGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCAAGGTTGAGATACAAGA
CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACGACTACTGCGAACAGATGTGGCACAGGGAGAAAGCG
GAGCAGAGAAACAAGGGGGCCCAAGTGGAAAGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTTAGTTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACAGTTTT
CCAAGAACAATCTTGACAAGCAAAGTATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTTGGAAATTTATTGTGATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT
GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGACACACAAATTAAGACAACCTCCCATATC
AACAGGAACCTTTCTCAGTGAACCATTCCTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATCTGGCTTTGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTTCAGTATATATTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTTTCTTTTACTGC
CTTTATCTCTCTCTGTATTTGATTTTGTGATTATTTTGAATGATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATTTTGTGAATTAACAGAACGAGTGTAAATTTAAC
AACGGAAGGGTTAAATTAACCTCTTTGACATCTTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAAT
GTAGTATTGTTTTTGAATTTAACAATAATAAGCCTGCTACATGT

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FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFLG
SSEGLDFQTLTLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPPQ
PFASVMTDEYLYSGTASDFLGKDTAFTSLGPTHDDHYIRTDISEHYWLNKAKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQORSLINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSVAVCVYSMADIRAVFNGPYAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPVAGGPTFK
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEELQIFKHSS
IILNMEISLQKQQLYIGSRDGLVQLSLHRCDTYKACADCCLARDPYCAWDGNACSRYPATSK
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGKPKWKHMQEM
KKKRNRHRHRLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

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FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTATCCTGGAGCATGCCACCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTACTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTATGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGTTGTATGGAGCTACAGAGGGGAGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTATGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTAAGTACAGGCTGGAGCAGAGGCGGCAGAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGTTACAGGAAGTCCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCCAGAGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAAATTTGGGGGGCGTGTGGGGTCTTCCCTCCCTGCTGGTGGAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCTTCTCTCTCCAGCTTCTCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTCTGG
ACATGATGGCAGCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACA
CAGATCCCTCACCCTGAAGGCCAGGGAAGCCTTGACCCCACTGATGCTGCTGTCTCTTCAAGCTGTCTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCTCCAAGGGT
GGAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCATTGTTCTATCATCTCTAGGACC
GGAACCTACTACCTTCTCTTCTGTATGACCCATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTTCTGCCCCACCTCTTCCCCACCTGGCTCCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGGCTCTTGTG
CTAAGAGGGGAGGGGGCTACGGTGCTATTGCTTTAGGGGGCCACCAGGGCAGGGGCTGCTCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGCGGGGCGAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGCACTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAAACTGTTGCTTCTCTCAAGCTGTGTCCAGC
TTTTCCCTTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCATTGCTCTTGAAGTG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
GGTCTGTCCCCACAGAGCCCAAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCTCTGACCAGGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGGAGGAGGGAGTGAAGGTAACATTTCCATTCCCT
TCATGTTTTGTTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGAGCCCAATTTCCCAAGCCCCATTT
TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

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FIGURE 350

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQEERLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESQSDNPCGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
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FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGAAAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGAGTCCCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCCCTTAACGGTCCTCAGCCCTTCTGAAAACCTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCCAGACAGGCTCGCATCCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGAGAT
CGTGTTCAGAGAAAGCTCAACGGCAGCGTCTGCCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA
CCTGGGCGAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAATCCA
CCTCCAGCCCCCTGGAGGGAGGCCCTAACTCTGCTGGGGGACCTGAGGGCTCACATCCTACGCCGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGCCCCGAGAGGAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTCAAGCACCCAGCATCCGCAATCC
TGTCAGCTTGGTGGTGAAGTCCGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCAGTGCTGC
CCAGACCCCTGCGCAGCTTCTGTGCCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCAGACACGCTGGGTATGGCTGATGTGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAAGTGGGTCACTGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCTTTGAGCAC
CTCTCGCCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCTGCTT
CATCACTGACTTCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGGCAGCTGACCTTCGGGCCCCGACTCACGCCATTGTCC
ACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCCGACAGGCTGCATGGGTGGTGCCTGCCATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCCTGGGGACCATGGGGTGAAGTCTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTCTCTCGCTACAC
AGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCCAGGCCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
CTGTGATCGCATCATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATCAGGTACGGATACAACAATGTGGTCACTATCCCCCGGGGGGCCACCCA
CATCTTGTCTCGGACAGGGAACCCCTGGCCACCGGAGCTACTTGGCCCTGAAGCTCGCAGATGGCTCCTTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGTTGCGCTA
CAGCGGGGCACTGCAGCCTCAGAGACACTGTCAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTTCTGCCCCGGCCGACCCCTTCAACGCCACG
CCCCACTCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCCGGCGCGCCCTGGGCGGGCAG
GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCACTGATGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTCACAGGAGGAGGGGGAAGGCAGGGAGGGCTGGGCC
CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTCTC
TTCCTGAATTTTATTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCTTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTCTTTCTTTCTTTCTTTTTTTTTTTTGTAGACAGAACTCTGCTCTGTGCCCCAGGCTGGAGTGAATG
GCACAATCTCGGCTCACTGCATCTCCGCTCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTGTGTTTGTGTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTAGCTCACTGCAACCTTCGCCACCTGGGTCCAGCAATTCTCCTGCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCGCCGCTAATTTTGTATTTTAGTAGAGACGGGTTTAC
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTCATCTCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACCGTGCCTGGCCAGCCCACTAATTTTGTATTTTGTAGTAGAGACAGGGTTTACCATGT
TGCCAGGCTGCTCTTGAATCCTGACCTCAGTAATCGACCTGCCTCGCCCTCCCAAGTCTGGGATTACAGG

FIGURE 351B

TGTGAGCCACCACGCCCGGTACATATTTTTTAAATTGAATTCTACTATTATGTGATCCTTTTGGAGTCAGACAG
ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTTGTGAGGATTAAATAATGTAAATAAGAAGCTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAA

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FIGURE 352

>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492.

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLHLQPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFA SLR FVETLVVADDKMAAFHGAGL KRYLLTVMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQ RGLNTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVC DPARSCAIVEDDGLQSAFTA AHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMA PVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTR PVPRNGGKYCEGRRTFR
SCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDGS GCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSP TDVVLPGA
VSLRYSGATAASET LSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPQDWLH
RRAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

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FIGURE 353

GC GGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGGCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTCAATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCTGC
TTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAAATATAAAGTGAAGTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

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FIGURE 354

MASTAVQLLGFLLSFLGMVGTLLITTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSLSLIGGTLLCLSCQDEA
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 355

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAAACATGA
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCG
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTG**TAA**TGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCAAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAA
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTAGACAG
ACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG
AAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTGTCTC
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTCGCGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAATAA
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCCAGAAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCAGCATTCCGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

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FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734 .
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1 . . .
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

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FIGURE 357

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG
CTGTTTCTTGGTGGTGGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
GTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATG
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT
GTGAGCTGGGTGGCAATGCCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGTGATTGTTGGA
GGAGCTCTGTTCTGCTGCGTTTTTTGTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
CCTTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA
AAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTACTGTTCTTAACTGC
CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGCAGAA
TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
TTCAAGCATCTACTCTTTTATCATTACTTTCAAATGACATTGCTAAAGACTGCATTATTTT
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA
CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT
AGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG
TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAATGAAGGCTTTAA
TCAGCATTGTAAAGGAAATTGAATGGCTTTCATGATATGCTGTTTTTTAGCCTAGGAGTTAGAA
ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
TTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAAGTCTTTTCCAGGGGCTATACTC
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAATATTTTT
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAAGTTT
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTT
CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
CCAAATTTGATGAACTGACAAATCCAAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAAT
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

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FIGURE 358

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIVVFENFWEGGLWMNCVRQANIRMQ
CKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

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FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACCTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTGAGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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FIGURE 360

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFLG
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDYYQRHYDED
SAIGPRSPYGFRRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

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FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG
GACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC
TGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGCATCCACTGCGCAAAAAGGATTGTGTCC
GGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAAGGCCGGCCACTCTCC
TACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGACCGTGGAGTCATTCCA
AGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCACTTCATGTTAT
TTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG
CTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG
ACCACAATAAAGAAATCTTTATATTTATCG

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FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNNLAGIHCAKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

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FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGGGAAGCAGGTCTTGACACGCTGTTG
GGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGGGAAGCAGGTCTTGACACGCTGTTG
GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGTTGCACCCCTC
CCCACCACACCCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTACTGCGGGAGGATCAGTGTCTGGTGGCCG
TGGCCTTACCCCAGGCCAGAAGGAACCAAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACAGCCTGGACCACGTGGCCTCCAGGAGG
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGCCTTCTGAAGG
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
GCCACCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTCGCTGCGAGGTGGTGAAA
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAATCAGGATTCCCATTTCCCCCTCGACCAGGAGGCCACCCTGA
GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC
AAAGGAGACTGGGTTGTCGGACATTCCTACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCAGTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCCACAGCACC
TGTGCTTTGCTGTCAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGCGGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTGAG
AAGGAAAAGAGAATTTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGTCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTACACCTTATTTTATTGACTGCTGGCTGCTTA

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FIGURE 364

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760 .
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGEEYSPLLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSVIDVI
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFHWFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWDQFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER
```

Signal peptide:

amino acids 1-28

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FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCCATGCGACCCAGGGCCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG
AATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

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FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 367

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAA

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FIGURE 368

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP
PAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

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FIGURE 369

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG
CTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAGACTCGCACGTCG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC
TGTCCTTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCACCTGGCTGTCTATCGG
GTAGGGCGGGGGCCGTGGGTTTCCAGGGGCGCACCCTTCCAAGCCTGTGTCCCACAGGTCCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACATACATAAATACTGGCACAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTAGTATGTGTGGG
CACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCTCAGCTGG
AGGCGGGCATCTTTCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCA
CATTGCCTTTTCCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGAGAGAGGAGGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCAGTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCCCTTCGGACATCCCAGGCACGAGGGTGTCTGGATGTGGCCACAC
ATAGGACCACACGTCCTCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399 .

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

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FIGURE 371

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTCAGCAGTGA CTGCCCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC
TCGGCCACGGCTGGGTTCGGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCCTGAGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTAACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCAACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAAA

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FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522 .

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 373

GA CTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAAC TGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCTGCCCCGTGCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
AACATCATTGACATAAAGGTCAGTACCCCCAGCTGCTGGAACCTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCAATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

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FIGURE 374

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPFALPLSPTGLAGSLTNALSNGLL
SGLLGILENLPLLDILKPGGGTSGLLGGLLGKVTSTVIPGLNNIIDIKVTDQPQLELGL
VQSPDGHRLYVTIPLGIKLOVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

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FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAATATGTCAAGATCCAGACTTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTGTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCAGTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTTGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

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FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303 .

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

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FIGURE 377

CGCGGATCGGACCCAAGCAGGTGGCGGGCGGCGGCAGGAGAGCGGGCCGGGCGTCAGCTCCTCG
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCC**ATG**GCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCC
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCTACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCGCTGACACCCTGCTCTCAGGCAGC
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATAACCACTTCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG
TGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGGCTTCTTGT
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAAAAAA

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FIGURE 378

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCA RTVG NIEELAAECKSAGYPGT
LIPYRCDL SNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

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FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGACCGTGACGAGAAGCCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT
CAAGTTACCATTTTTTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTACAATCTC
AAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTGGACTCATTTGGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAACCTAATTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGCTTTTCAAGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACCTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCATTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAATCATTCTGTCAATTTGTTCTC
AATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTCACATACAT
GAATGTTCAATTTAAAAGTTTAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAAATAAGAACATTTAAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAAGTCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

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FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP

VTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

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FIGURE 381

AACTTCTAC**AT**GGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAAGATTCCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAAT**GA**GGAACTGAGAAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACATCAAACAT
TTATTTTTTATTCTTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAACCTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAATAACCACACATGGCAAAAA

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FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQ
PVKGHGTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTACCTTCAGAACA
ACCAAATAAATAATGCTGGGATTCCCTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
ACCTATACCACAACAGTTTAGATGAATTTCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCTATCTGG
AAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCGGAG
ACAGCAACTATCTCCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAAATTCCTGGGGTT
TGCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT
CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTCT
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTTCATA
TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATA
GCCCAGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACCTTTGG
CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT
ATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCA
TATTTCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

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FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK
IPYLEELHLDNNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDL DNITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPDIKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCJETETAPL
RMYNPTTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSES
SSNRSYRDSGIPDSHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

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FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG
CAGCCCTGCCGGGGCCACTTGTCTTCA**ATG**TCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
GCAGAGGCCCGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGCGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCTCCAGCCCCGGTTTTTGGAAGCTCCCATATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTTCGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCACCAACTGCTCTTCTCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCCTACCCG
GGACATCTTCATGGAAAAATCATGTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCTCATCCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTTATATTTTTTTAGTAGAGAC
AGGGTTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC
AGGCTCCCAAAGTGTGGGATTAT**AGG**TGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAAA
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTCTATACA
TCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

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FIGURE 386

MSARGRWEGGGRRACRGS LGLARAQGAERTVSSEQRPAMASLG LLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQ RSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPO
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCGFGEFDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSC LILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

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FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTC**ATG**GGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAGGAGG**TAG**TCAG
GCCGTCCAGAGCTGGCATTGTCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGGA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAA
TTATATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 388

MAAALWGFFPVLLLLLLLLSGDVQSSEVPGAAAEAGSGSGVGIGDRFKIEGRAVVPGVKPDWIS
AARVLVDGEEHVGLKTDGSFVVHDIPSGSYVVEVVSAPAYRFDVVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSSKTGKSGAGKRR

Important features of the protein:**Signal sequence:**

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

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FIGURE 389

GTCTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCCATGGCGTGGAGCCTTGGGAG
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT
TATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
CCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
GGTCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
CCTCGGCTGCTTCTCCTTGCTGGTGGCTTACAAGAAGACAAAGTACGCCTTCTCCCTAG
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
TTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAGTGTATTGCAGAAGA
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCGCTGGGCAGGG
GCCCCAAAGCTAGGCTCTGAGAAGGAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGA
AAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCATGATGTTTTCAGAAGTTGGC
CACTGAGAGTGTAATTTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTGAGGCAGGCGG
ATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
GCTACACAGAGCACGGACTTTTGGATTCTTTCAGTACTTTGAATTTATTTTCTACCTATAT
ATGTTTTATATGCTGCTGGTGTCCATTAAAGTTTTACTCTGTGTTGC

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FIGURE 390

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMVAVILMASVFMVCLALLGCFSLLWCVYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSL
GTPPGQGPQS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

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FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCC
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAAAT**TAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACCTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

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FIGURE 392

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

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FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCACACCCCTGCTGGAGTTCTACTTGAAAAGTGTTCACAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAGTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**GA**ATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGATTTTATTACAACCTCTATTTAATTAATGTCAGTATTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAACTCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAACAGAGAGGGATG
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAGTAAACGATAAAATGTGGATTAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCATTTCCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAA
AAAA

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FIGURE 394

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGGQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL
```

Signal sequence:
amino acids 1-42

N-glycosylation sites.
amino acids 85-89, 99-103, 126-130

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FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCACTGAGTCTTAGTTTTATTTTT
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGGT

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FIGURE 396

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGACGGTCTATCCTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAAC**TGAT**GCCACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCAAGTGTCTGTGAGAA

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FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDPKTVIEYDYVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP
QLQDLDPQAQHTDSEEGPEEPPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

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FIGURE 399

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACCTAGTGTGCAACAGGGGAC
TATTCAATTTTGTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTATTGGGGCCCATAATATTCCTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAAATGAGGAGACAGTAGAAGTGAACCTTCAACAACCTCCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG
ACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTTGCAGAAGTGAGGTCACTCTTGAAGGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

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FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLDLRVEPVTTSVATGDYS
ILMNVS WVL RADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP
YFPTCGSDCIRHKGTVVLCPTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQVSAGKRSQACHDGCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

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FIGURE 401

GGGAACAGGGAACTATCAGCCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG
GGACCTTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCCG
GGGCCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTCATCTCCAAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTCGGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAAACTGGTGACATCATTTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC
CGCATCTTGGGCTTTAAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCAATTAGAAAATGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTCTGGTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCAGAAAGGCATTCATCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTCATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAAACAAAAAATTA AAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATTATTTTATGAATTTACTGT

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FIGURE 402

MDRDLRLQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPPQHPLQGRKEKRVD
NIEIQKFISKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSHGDP
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGSNLKA
IEDFELALENCPTHNRKYLQCTLVERGGQLEEEEEKFLNAESYYKKALALDETFFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQTKKIETSAEKLRLKLLKEEKRLKKRRKSTSSSS
VSSADESVSSSSSSSSSGHKKRHHKRNRSSESSRRHSSRRASSNQIDQNRKDECYPVP
ANTSASFLNHKQEVKLLGKQDRLOQYEKTOIKEKDRCPLSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

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FIGURE 403

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTTAGCCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTCCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCCAACTGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTTCAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCAAGTGTTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAAACGATGAAACTGCAAAA

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FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPOYPLLIIVVYK
VLATLGLILLTAYFVIQPFSPPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFFPYPWRRPLNRSQMLRELFVFTHL
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC
GTCTCCTCCTGTCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
CAGCGGACGACCCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGG
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG
TAGCCCGCTGCCCGGCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAC TAGTC
ATGGTGCTGTGGGAGTCCCCGCGG CAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
CCCGTCATGCTACTCATCGTAGCCCGCCCGGTGAAGCTCGCTGCTTCCCTACCTCCTTAAGTGACTGCCAAACG
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA
TTTGATGGGGAATGTTTAAAGAATTGGAGACACTGTGACTTGCGTCTGTCAAGTGCAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAAACAGCAGAGT
GAGATACTTGTGGTGT CAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGT CAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAAC TACAAC TACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGTCCTGTACGATTT CAGTATGTCTTAATCGCAGCTGTG
ATTGGAACAATT CAGATTGCTGT CATCTGTGTGGTGGTCCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTCAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
AGGGAGCATGTTT CACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCTTGCAATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG

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FIGURE 406

MVLWESPRQCSSWTLCGFCWLLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTT TK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTRASTRLI

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FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCATTTTTAA
CATTCCTCCTCCAATTGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCGTGTCTCTCCACGACT
CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC
CGAGCTCCTCCGGGGGTCCCGCCCGAGCCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGACATGCCAGGAATAAAAAGGATACTACTGTTACCATTCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCTACTCAGGTCCTGACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATAACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCACCCAGATCTGCA
TCAATACTGAAGGCGGGTACACCTGCTCCTGCAACCGACGGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTCGCTATGGTTACTGCGCAGCAGCTCTGTGCGAATGTTCTTGAT
CCTATTCTTGATACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGCTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTTATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCTG
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCTGACTCTCACCTGTA
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCTTATGACACAGTTATCAAA
AAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGGGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTCGTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGC
CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAATTCT
GTCTTGTTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCAATTGGATTGGAATGCAGAGGTCT
CCAAACTGATTAAATATTTGAAGAGA

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FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQN
GGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCV
DVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYS
CTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSGLICRCDPGYELEEDGVHCSDMDECS
FSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI
DPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAY
YIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI
YVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTCA
GGGAGGAGCACCGACTGCGCCGACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
TCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGAAGAGT
TATGCCGGCTTCCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGACCTTGCGT
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
GGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCAGGGAT
TTATACAGTGCACATAATTCAGTTTTTCCAGATATTTCTGAATATAAAAAATAATGACTTTTAT
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG
CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
TTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTTGGGTTGCACGGAACCTGAGGAT
CAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
CAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCGAG
GAATACAAGAAGGCAGAAAAAAAAGTTTGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
TACATCCGGAAGCGGGTGACTTCCATCAGGTAATTATTGAGGTGGAGGACATATTTTACCC
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT
CCTTATGTTGGATAAACTACCTTCCCAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTGTTTTGGGGGGAGATGTTTACT
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTTA
ATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTGTAACAAACAAAGCTGTAACATCTTTTCTG
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

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FIGURE 410

MVGAMWKVIVSLVLLMPGPGCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKGRELSLV
GPFPGNLNMKSYAGFLT VNKT YNSNLFFWFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F F Q I
FPEYKNNDFYVTGESYAGKYVPAIAHLIHS LN P V R E V K I N L N G I A I G D G Y S D P E S I I G G Y A E F
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNV TGCSNYY
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVG N Q T F N D G T I V E K Y L R E D T V Q S V K P W L T E I M N N Y
KVLIYNGQLDII V A A A L T E R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q A G D F H Q V
IIRGGGHILPYDQPLRAFDMINRFIYKGWD PYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

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FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCGAGCCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGTGTGCCCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGAGCCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCAGCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCTCACCTGCCTTAAGCTGTGGTACAACCATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCTGGAGCTTGCTCTTCACTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAGCAGCCAGACGT
TGAAGTGTGTTTCTTCCCTGGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCCTGGGAGGGAGGTTTTTTTTGTTGTTTTTGGTTTTTTTGGTGTCTTGTCTTTCTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCTCATTGACCTCCCTCCTCGTGCCTGCCCTGCCTCTCCA
CGCACAGTGTAAAGAGCCAAGAGGAGCCACTTCGCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGTTCCCGCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTTGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTCACAGTATCAATAAA
ATCTATAACAGAAAAA

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FIGURE 412

MRQTIKVIKFIILICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLS GIPDTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTTCATATGAGGAAATAAGTGGTAAAATCCTTGGAATACAAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGATTTTC
ATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACAGCTGGATCTCA
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA
TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAAATCAGATTTCCAGAAAATGCTCATCTGCATCTAAATACTGTCTCTTAGGAT
TCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAACAAAACCTGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTTGCGTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACTTTTCAAGATCTGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCAACAAATTCATTTGACTACTCAAATACTGTAATGA
GAATATAAAATTTGGAGCATGTACATTTTCAAGAGTGTGTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGGACAAAATGGACATAGAAAACCTGACAATATCAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTTCAATATTTAAATTTTGCCAATAATATCTTAACAGACG
AGTTGTTTTAAAAGAACTATCCAACCTGACCTTCACTTGAAGAACTCTCATTTTGAATGGCAATAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACACACACCCCTTGGAACACTTGGATCTGA
GTCAAAATCTATTACAACATAAAATGATGAAATTTGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTATACATAAAATTTGTCTGATTCTGTCTTCAGGTGCTTGCCCAAAAGTATTCAAA
TACTTGACCTAAATAATAACCAATCCAACTGTACCTAAAGAGACTATTCATCTGATGGCCT
TACGAGAACTAAATATTGCATTTAATTTTCTAACTGATCTCCCTGGATGCAGTCAATTCAGTA
GACTTTTCACTTCTGAACATTGAAATGAATTCATTTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTAA
AAAATTTTCACTCAGCTTGAACATATTCAGAGGTCTATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCCCTTAAACCTAAGGGGAAGTAAAGACGTTTCACTCTCCACGAATTTAT
CTTGCAACACAGCTCTGTTGATTGTCAACATTTGTTGTTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCACAGGGTTAGGAAAACAACCCAAGAACAACTCAAGAGAAATGTCCGATTCCACG
CATTTATTTATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTTGCTTTTATGAAAGCTACTTTGACCTGGCAAAAGCA
TTAGTGAAATATTTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCCAACCAATCTCTTCCATG
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTCCACCA
GGTATCATAAACTGAAAGCTCTCCTGGAAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAACTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATAAAATCCACAGTCCCTTGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACTTTATGATGGCAATTTGACAATATTTATTAAAAATAAA
AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAGGTTGTTTATCCAGGATTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGAATCCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACT
AAAAATACAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAACATCCTCATGGCCACAAAATAAGGTCTAATTCATAAATTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAA
CATATTAATATTGTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGGCATTGAAA
TGGCATTGAAATAAAGTGTAAAGAAATCTATGCCAGATGTAGTAACAGTGGTTTTGGGCTGGT
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTGATTTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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FIGURE 414

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN
TTKLHIVLPMDTNFWLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFIQ
QDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFAANNILTDELfKRTIQLPHLKTli
LNGNKLETLSLVSCFANNTPLEHLdLSQnLLQhKNdENCsWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDlnnnQIQTVPKETiHlMALRELNIaFNfLTDLPGCSHFsrLSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGWSDSYTCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHhNLFHENSdHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

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FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCTCCCCCGC
TTCCCTGTGCGGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGAGGTGGCGACAGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGGGCGGCGGACGGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCTGGTCCGGGACAGCCGACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAACCTACGCTCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCTGCAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCTCCCTGCTTGCATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCCTGGATATACACCTAGCCTCAGTCTCCCAACCCCACT
CCTGCCATTGGCTGTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCTGAGAGCTCCCGACTACTGCGTAGTCTACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA
ATGGTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGTGGCACCT
CTGGTGCCACAGCCTGTACCTGCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTGCAACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGCTCCCTCGAA
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTCAACCTTCTGCTGCTCCCTTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA
AGGCTCCCTCCCATCTGCTAGCACGTCTCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGACGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCTCTCCCTGGGGGCTTACTCATAGTGGCACAACTTTTAGAGGTGGGTGACCTCCCTCC
ACCACTTCCTTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCCTCCCGTTGACCTATGTAGCTGTATATAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTGTACGTGGCCATGGCCAGACCCCACTCCCT
TCACCACCACTGCTCCCCACGCCACCACCTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

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FIGURE 416

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPVLRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFFGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG
PGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCDKCVYETWVCDGQPDGDCADGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYQQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRIMRRLVRRLLRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPTSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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FIGURE 417

GTCGTTCTTTGCTCTCTCGCGCCAGTCTCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCGAGGTGCTGAGCGCCCTAG
AGCCTCCCTTGCCGCTCCTCCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCGAAGCAGCCGCCGATTCCAGCTGCCCGCGCGCCCCGGGCG
CCCCTGCGAGTCCCCGGTTAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC
GCCGCGGAGCCACAGCCACGATGATCGGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACCACCACAGCTCAG
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATAACGGTGTGCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTGATCAAGCGGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGTCTTTC
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTTTCTGCCTCTGTTAGACCAAAGGTAAGT
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCCTGCTGCTGGTGCTTGTGGTGATTGTGGTG
TGAGTATCCGGAAGCTCGAGGACTCTGAAAAGGGGCCCCCGCAGGATCCAGTGCCATTGTGAAAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTTGCTGCTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCCG
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCCAACTTGAGAATTCGGCTCTCCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGAC
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTTCGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
ATTTAGTGGCAGGCTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTCTTTTCTCCTTCTC
TCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCTTCTTATGTATTTCAAGATTATTCTG
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTACTATTATTTATTTATTTGTTGCTTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA
CCCCATTGAGTTACTGTAATGCAATTCACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTTCAATTCATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGTTTTACCTGGACACCGTGTAAGTGTGTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAAGTGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGATTCTTCCACCAATT
ACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGTTTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAACATTAGGTGTTTGTTA
AAAAAAA

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FIGURE 418

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVPGGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGPHHRHILKLLPS
MEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQL
ETDKLALPMSPLSPSPPIPSNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCSTSSGS
SALSRNGSFITKEKKDVLRLQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLLDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

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FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACAGTCTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTCAACATTGGAGTTGAGTACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCACTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTGGTCCGTCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG
CACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCAGAGTGACATGAGTACAGACCCCTCCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCT
GCCTGGAAGAGGTCTGGGTGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

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FIGURE 420

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRD LIEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFT VYISADSKSSNSNVIQVDQSG LFLPSRDY YLNRTANEKVL TAYLDYM
EELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVGMDYLQQVSELINRTEPSILNNYLIWNLVQKT TSSLDRRFES
AQEK LLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA F
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY
NFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

Type II Transmembrane domain:
amino acids 32-57

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FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGCC
GCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA
GAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCCCTCGGGAAT
CACAAC TGGGTACAAGACATTTGCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTCAGCT**TCAG**CTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTTCGTGG
GCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCGGGACCCCCCTGCCTTCCTGC
TCACCCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 422

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSSLGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS

Signal peptide:
amino acids 1-42

Transmembrane domain:
amino acids 29-49 (type II)

N-glycosylation site.
amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 27-31

Tyrosine kinase phosphorylation site.
amino acids 226-233

N-myristoylation site.
amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGATC
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATGCT
GCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAACCTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCCTTCTTTTTCCTT
TTTCTTACCTTCATTTACAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSIVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:**Signal peptide:**

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 425

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAA

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FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQH
YRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSGKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTCCTTCACTA
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTGAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG
AGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
GTTTCAAGGAGACAGTGACAATTGATAATGAAAAAATAACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATAACACCTGGGTCAAG
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAAGTCAAATTAAATTCTTTCCAATGCCCCAACTAATTTTGAGATTCAAGTCAGAAAATA
TAAATGCTGTATTTATA

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FIGURE 430

><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIIFIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

Important features:**Signal peptide:**

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

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FIGURE 431

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT
TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 432

MSRSSKVVLGLSVLLTAATVAGVHVKKQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

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FIGURE 433

GAATTCGTGTCTCGGCACTCACTCCCGGCCGCCGGACAGGGAGCTTTCGCTGGC~~CG~~CGCTTGGCCGGCGACAGGA
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
CGCTGCCGCTGCTGCTGGGCCTCTTCTCCCCCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA
AGCCTTACCCGCTATTCCCGGGACCTTTTCCAGGGAGCCTGCAAACCTGACCACACACCGCTGTTATCCCTTCCTC
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTACCAACCCAGCCTGGAGACCACATACAGGAAACGTAGCCATT
CCCCAGGTGACCTCTGTCAATCAAAGCCCTACCGCTCTTGCCTTCAAACACACAGTTGGACACATAATACTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
TGGAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCCCTTCAGCATAACCAGTGTGCAGCGTTCAGACAATGGGTCGTATATCTGTAAGATGAAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCTCACTTTACTAAGCAGCCTGAGAGC
ATGAATGTCAACAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCGCTGAGCCCGTCAACATTTTC
TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGGCGTGCTAACTGTTCCAGGCCTGACG
GAGATGGCGGTCTTCAGTTGTGAGGCCACAATGACAAAGGGCTGACCGTGTCCAGGGAGTGAGATCAACATC
AAAGCAATTCCTCCCCACCAACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
CCTGGTTTTGATGGATACTCCCGTTTCCAGGAATTCAGCATTGAGGTCAAGGAAGCTGATCCGCTGGGTAATGGC
TCAGTCATGATTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTGGTGTCTTCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGACTGAA
GGAGCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGTTGGCAGAGTGACAGG
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAGGATTGCAGCCGTACCCAGAGGGGGAGTTGGGCCCTTCAGTGATCCAGTGAAAAATATTTATC
CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCAACTCCGGCGCTGGCAACGCAGATCCTGTGCTCATCATC
TTTGGCTGCTTTTGTGGATTTATTTTGATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAAAGAAATCCTTC
TGTCGGCGAGCCATTGAACCTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAAGTAGAAGATGTT
GTGATTGACAGGAATCTTCTAATTCTTGGAAAAATTCGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTCTTACATCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTCATGAAAGACTTCAGCCACCCAAATGTCATTGACTTCTAGGTGTG
TGTATAGAAATGAGCTCTCAAGGCATCCCAAGGCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
ACTTACTTACTTTATTTCCGATTGGAGACAGGACCAAGCATATTCCTCTGCAGACACTATTGAAGTTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTGCGGACTTCGGCTCTCTAAGAAGATTTACAGTGCGGATTATTACC
CAAGGCCGATGCTAAGATGCCTGTTAAATGGATCGCCATAGAAAGTCTTGCAGACCGAGTCTACACAAGTAA
AGTGATGTGTGGGCTTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCCGAAGACTGCCTGGATGAAGTGTAT
GAAATAATGTACTCTTGTGGAGAACCGATCCCTTAGACCGCCCCACCTTTTTCAGTATTGAGGCTGCAGCTAGAA
AAACTCTTAGAAAGTTTGCCTGACGTTCCGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCAGGGCCCCACCCTTGTCTCACTGGACTTGAACATCGACCCCTGACTCTATAATTGCCTCC
TGCACTCCCCGCGCTGCCATCAGTGTGGTCACAGCAGAAAGTTTCATGACAGCAACCTCATGAAGGACGGTACATC
CTGAATGGGGGAGTGAGGAATGGGAAGATCTGACTTCTGCCCTCTGCTGCAGTCACAGCTGAAAGAACAGT
GTTTTACCGGGGAGAGACTTGTTAGGAATGGGGTCTCCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA
TTGCCGATGAACTTTTGTTTGTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA
GACATTCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTGTCTT
CCTTACCAAGTGAACCTCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA
TATATATTTATTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAATAAAACATTACTTA
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTCAACTTCTTTTCTTTTCTTACTATTAATGTAAAAATATTTGTAATAATGAAATGCCATATT
TGACTTGGCTTCTGGTCTTGATGATTTGATAAGAATGATTAATTTTCTGATATGGCTCCATAATAAAATGAA
ATAGGA

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FIGURE 434

MGPAPLPLLLGLFLPALWRRRAITEAREEAKPYPLFPFPFPGSLQTDHTPLLSLPHASGYQPALMFSPTQPGRPH
 GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNCSSINVPNIYQDTTISWWKDGKELLGGHHRITQFY
 DEVTAAIIASFSTSVQSRDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE
 PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCEAHNDKGLTVSQGVQINIKAIKPSPTTEVSIRNSTAHSI
 LISWVPGFDGYSPPFRNCISIQVKEADPLNGSVMI FNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
 ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQDQDGLVGYRISHVWQSAGISKELLEEVGQNGSRARISV
 QVHNATCTVRIAAVTRGGVGPFSDPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCFCGFIILIGLILYISLAI
 RKRVTQETKFGNAFTEEDSELVVNYIAKKSFCRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS
 VMEGNLKQEDGTSKLVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIKPMVILPFMK
 YGDLHTYLLYSRLETGPKHIPLQTLKFMVDIALGMEYLSNRNFLHRDLAARNCMLRDDMTVCVADFGLSKKIYS
 GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGVMTMWEIRTRGMTYPYGVQNHEDYLLHGHRLKQPEDC
 LDELYEIMYSCWRTPDPLDRPTFSVLRQLQLEKLLSLPDVNRQADVIVNTQLLESSEGLAQGPTIAPLDLNDP
 SIIASCTPRAAISVVTAEVHDSKPHEGRYIILNGGSEEWEDLTSAPSAAVTAEKNSVLPGERLVRNGVSWSHSSML
 PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

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FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGGAT
CCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCTTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAACTCTTTGGATATGTGCATCAGTGGTTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTGATCACTTATATCTGGAAACC
AAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTTATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGCATCCAG
AGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACCTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTCAGAGGAG
CCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

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FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRC LSS
KSC EGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQAK
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFDPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP CSATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP CPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKEKLPVEAK
LPWFKQAQELEEAAVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTACAGGACATTCGC
CCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAAGGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAACTAACA
ATGTAGGTACTAGTGAATACCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

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FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH
RNHLCFCDLYDRATSPPLKCSLL

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FIGURE 439

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAAGAGTGGAGTGTGGCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTCACACTGGCTTGCTCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGAACCTCCA
AGGATGAATGTAACCTGGCGCCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCTATCACC
CACGGGACCCCTCGTCATCACTGCCCTTAACAACACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGCG
GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
ATTGAAGTGGATGAGGGAACACAGCAGTCAATGGCTGCCACCTGCCGTGAGAGCCACCCCAAGCCAGGTCCGG
TACAGCCTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACACC
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGCC
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTTGAGTGTGTGGCCAGTGAATCCCACCCCCACGGGTC
ACCTGGGCCAAGGATGGGTCCAGTGTACCCGGTCCACCAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
ACCACGAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCGGGCAGCGTC
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTTCATCCCTGGGGC
CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCCC
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCTCAGCATGGGGCCTGAGGACGAGGC
GTCTACCAGTGCATGGCCGAGAACGAGGTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGGGCTCCCGAGACCCCAACGTGAGTGGGGCTGCTTCCCGAAGTGT
CCAGGAGAGAAGGGGAGGGGGCTCCCGCCGAGGTCCCATCTCCTCAGCTCGCCCGCACCTCCAGACGAGAC
TCATATGAAGTGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC
CGCAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGCCAAACAGCACCGCCTGACCCCTC
ACCAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGTGGCAGCTTACAATGTGCGGGAGAGGGCCAGACAGCC
ATGGTCACCTTCCGAAGTGGACGGCGGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGC
GACCTTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCGCCGCTCTCCCCCAGAAGCTCCCGACAGG
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTAATC
CAGTAACTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACACGCGCTACCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGCTACAGCGGTGCGGTGTACGAGAGG
CTGGTGGCAGTCTCTTATATCACCTTACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTCAATGATAGT
GACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC
GACATTAAGATGCAGTGTTCATGAAGGAGGGGAGAGCGAGTTTCAAGCAACGTGATGATCTGTGAGACCAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGGCACCCTCACTCTGGCCCCACACAGCCGCCCCCTTCTGAAACC
ATAGAGCGGCGCGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC
CTGGGCTCCATCGTTCTCATCATCGTCACTTCTATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAACAT
ACAACAGACCTGGGTTTTCTCTGAAGTGGCTTCCACCTCCTGCCGTATACTATGGTGCCATTGGGAGGACTC
CCAGGCCACCGAGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCTCGGCTGCAGTGGGCTACCCGGGATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCATCTTGGCAATGGATATGACCCCCAAGTACCAGATC
ACGAGGGGTCCTAAGTCTAGCCCGACGAGGGCTCTTCTTATACACACTGCCCCGACGACTCCACTCACCAGCTG
CTGCAGGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC
CCCGACAGTCTGTCTTGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAAGTGGAGGAGTGGTGTCCCAGCACCCGATAGGG
GCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGGTGTGCTTTTGAACACCACT
CTCACAATTTAGGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA
AGAGACAGAGAAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTGGAGAGGGAAAAATAAAGAAAGCTGCCA
CCTAACAGGAGTCAACCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATACGAGCA
TGAGGGAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA
ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAACCTTCCAGAAT
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

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FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGI PPPRV TWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGP GAAVILY
NVQVFEPPEVTMELS QLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCM AENEVGS AHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLLTLRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRVRALNMLGESEP
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNTPIHGFYIYYRPT
DSDNDS DYKKDMVEGD KYWHSISHLQ PETS YDIKMOCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VLIIVTFIPFCLWRAW
SKQKHTTDLGFP RSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSGPPCCLGLVPVEEVDSPD
SCQVSGGDWCPQH PVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

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FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTCTGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCCTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCTGGGAAACACTCTGAGATATATA
ACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

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FIGURE 442

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFERSDYISDEALES LPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGV NKDSL MPLW WNGSEPLWVT
LTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLA AIYH
ERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

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FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTC
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATAACCTAGAGTTCCTGTAGTGTCTACATTAAAAAT
ATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCCTCCTGCAGCTTGGACCTTTGACTTCTGACCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

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FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC
CCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGACGTGTATTATTAACTGATGAACACATCCCCAAA

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FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

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FIGURE 449

TGCAGAGCTTGTGGAGGCC**AT**GGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGGCCGCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCAATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAATTGGAAGTCTGAGACTCGTTCAGACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGCAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTTAAC
CACTGATAATTCAGATTTGTTCAATTAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCCGAGAAATGCCCCCTCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC
TGCACTCCTTGCTTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAACTGAAC**TGA**AGTGACACACTCCTTTTTTCCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

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FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCEGAELRAPFDKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGOEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMHMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGLMLNRTLLETLOKAGFSEKFLNEMIAFVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTGTKYTGNPTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGINTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSSIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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FIGURE 451

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAAATGG
CATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTCCC
CGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCAACCCCTGCCTCACAGG
TGTATTCCCTCAACACCGACTTTGCCTTCGCGCTATACCGCAGGCTGGTTTTGGAGACCCCGA
GTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCTTGGGG
CCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACACACCAG
AGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACCTCACTGACTGTTCCAGCAAAGACC
TGACCTTGAAGATGGGAAGTGCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGCAAATTTCT
TGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCAAACCCCTCCA
TTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTTGTAGACATAA
TCCAAGGCCTTGACCTTCTGACGGCCATGGTTCCTGGTGAATCACATTTTCTTAAAGCCAAGT
GGGAGAAGCCCTTTACCTTGAATATACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGG
TCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGC
TGAAGTGCCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCTCCCTA
GCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACACTGATAAAGTGGAGCC
ACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCCATTTCTGCCTCCTACA
ATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAAATGCTGATTTTT
CTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATG
TCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGG
ATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCTGATGATGATTACAAATAAAG
CCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCACTAAATCCTAGGTGGGAAATG
GCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCTCTTTCTGT
TCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTGCTGGCAGGGATGCCACTTCCAAGGCT
CAATCACCAAACCATCAACAGGGACCCAGTCACAAGCCAACACCCATTAACCCAGTCAGTG
CCCTTTTCCACAAATTCTCCAGGTAAGTAGCTTCATGGGATGTTGCTGGGTACCATATTTT
CATTCCTTGGGGCTCCAGGAATGGAAATACGCCAACCCAGGTTAGGCACCTCTATTGCAGAA
TTACAATAACACATTCAATAAACTAAATATGAATTCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 452

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

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FIGURE 453

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGCCCCGGGGCGACTCG
GGGGCGGACCGGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGCTGAACACATCTCCAACCTAC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG
GACGAGAAGGGGAATGTCTCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTGAGAGCCTGGGCGAGCTTGAAGGCGATGATGACCAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTTGTGTCCGCGATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTTCAAC
GTGCTGCAGGATGTCTTCAGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTTCTATGGGGTCTTCACT
TCCAGTGGCACAGGGGAACCTACAGAAGGCTCTGCCGTCTGTGCTTCAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCAACAGTGCCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCGTGCTG
AATTCTCAAGGACCACTTCTGATGGACGGGAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCTGGCTGTACACCGCTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCACTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCAGAATCTGCTCCTGGACACCCACAGGGGGTCTGTGTATGCGGCTCACACTCGGGCGTAGTCCAG
GTGCCCATGGCCAACAGCTGAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCCGGACCCCTACTGTGCTTGG
AGCGGCTCCAGCTGCAAGCAGCTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCGGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTCAGCGCGCTTTCGGTTGTGTCCCGCTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCAGCCCCAACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
GTCTGGCTACGCAACGGGGCCCCCTCAATGCCTCGGCCTCCTGCCAGTGCTACCCACTGGGGACCTGCTGCTG
GTGGGCAACCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTCCAGCAGCTGGTAGCCAGCTAC
TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCTTATCAGCACA
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCGTGCTGCTCCAGTTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCCCTTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATACCCGAGGGTACCAGTCCCTGTAGACAGCCCCCG
GGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCGGCCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGGTGAAC
ACGACCGTGGTGGCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCAACAGCCGTGGCCCCAGAGGTCTTGCCCAATATGGGGGCTGCCCTAGGTGGTGGAA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCAAATGTGAACTAGAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGTGG
TTGCTGAGACAGAGTTGGAAACCTCACCAACTGGCCTCTTACCTTCCACATTATCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTAGGACAGCTTGGGCTGCGTGCGTTCTGCCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACACCTCAGGGACAGAGGGTAGGTGGCACTGCGGCCCTCACCAGTCTCTGGGCTC
GGACCCAACCTCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCTTTCCCTCAGAATTGAGGGAAGAGACTGTGCGCTGCCTTCTCCGTGTGCTGTA
GAACCCGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTGAACCAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCGAGTCCCGAGTTACCCCTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTAATAAA
GTCTGAAGAATTACTGTTAAAAA

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FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962 .
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGGDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRPDD
GFPFNVLQDVFTLSPSPQDWRDTLFGYGFVTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAHSVSVGPRVHIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQQLATRPWIQ
DIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLVLVGTOQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDGGSPVPII
STSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAVS
HPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGCAGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTAAAGACCCAGCACCCCTATTCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCCC
GAGTGACTAACGTCTCTGTACACCGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCAGTCTGGCCAGTTTCCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTTCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTTCAAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAAGTACCCTTGCAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC
CAGGGTTTAAAGCCGGCCATGCCTTCCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCCTTGCCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCCAATCCCTCACAGCCTGACCCTCTCATTCATCA
GATCTCGTGCCG

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FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRWWVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

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FIGURE 457

CCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCGGCACAGCCGCCGGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCC
CTTGTGACCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGAGACCACACCGAGGACGGCTCAACATTCATTTCAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCTT
GAGGCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTTCAGCATCACAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTGGGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTCGACATGACTCGCACCCCGTGG
GCTGCCCGCGAGCTCACGCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCCTCAC
GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTTGGCGT
CTGCTGACCCCAAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTTCAGTGACACGG
AACTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTTCGTGCTACCAAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAVAVGPAVGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDFLEAPASGSSDPLDFQHH
NYKAMRKLKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYHRSSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGEVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTGDMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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FIGURE 459

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 460

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290 .
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW
FRNRFPIPIPIESAPTTPLPSEK

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

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FIGURE 461

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTGATGTTCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCTTCTTTTAAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCTACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCTCTGCTCTTTTAAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTTCA
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

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FIGURE 462

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAALF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL
```

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 143-162

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FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCC
ATGCTGCTGCTGCTCAGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTAGCACCCTGAAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGGACGTG
AACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTCGCCTTCCAAGCTTTCCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGTGCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

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FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFRLGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

FIGURE 465

CGGACGCGTGGGTCCGCGCGCCTGAGGCTGCACCGGGCACGGGTCCGCGCAATCCAGCCTGGGCGGAGCCGAG
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGT
TGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGTCTCAAGGACATATCCCTGGGC
AGCCAGTCACCCCGAGCTGGGTCTGGATGGACAACCCTGGCGCACCGTCAAGCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGC
TGGCCCCAGGATACATAGAAACCCTACGCGCCAGATGGGCAGCCAGTGGTGTGCTGGCCCCAACCCACAGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGTCACTGCTCTGGGATGAGTG
GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCCAGGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGGCATGACCAGCCTTCTTGGTGGTCCCCAGAGCAGGGGCGAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
AACTGTACATTGTGGCAGACCACCTGTTCTTGACTCGGCACGAACTTGAACCACCAACCAACAGCGTCTTC
TGGAACTCGCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTACAGTGCGCTGACCGGCTGGAGGTGT
GGACCAGCGGGACCGCAGCCGCTCACGCAGGACGCCAACGCCACGCTCTGGGCTTCTCTCAGTGGCGCCGGG
GGCTGTGGGCGCAGCGGCCACGACTCCGCGCAGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC
TGGCGCCCGTTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCTGAGCAGGACCATCGGAGCTCCCCATCG
CGCGCGACCCACCATGATGATCGGCCACAGCTCGGCTCAGCCACGACCCCGACCGCTGCTGCGTGG
AGGTGCGGCCGAGTCCGGAGGCTGCGTACATGGCTGCGGCCACCGGCAACCCGTTTCGCGCTGTTACGCGCT
GCAGCCGCGCCAGCTGCGCGCTTCTTCCGCAAGGGGGCGGCGCTTGCTCTCCAATGCCCCGACCCCGGAC
TCCCGGTGCCGCCGGCGCTTGCGGGAACGGCTTCTGGAAGCGGGCAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGGGACTGCT
CGGTGCGCTGCTGCTGAAGCCGGCTGGAGCGCTGTGCGCCAGGCGCATGGGTGACTGTGACCTCCCTGAGTTTT
GCACGGGCACCTCCTCCACTGTCCCCAGAGCTTTACTACTGACGCTCACCTCTGCCAGGGGACAGTGGCT
ACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCCACCCAGCTC
CCGAGGCTGTTTCCAGGTGTTGAACTCTGCGGGAGATGCTCATGGAAGTGCGCCAGGACAGCGAGGGCCACT
TCCTGCCCTGTCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
CGCACATGTTGCCATGGACTTACCGTTCCACTAGATGGCCAGGAAGTGACTGTGCGGGAGCCTTGGCACTCC
CCAGTGCCACAGCTGGACCTGCTTGCCCTGGGCTGGTAGGCCAGGACCCAGTGTGGACCTAGAATGTTGTGCC
AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTACGCGCTGCCTGACTGCCTGCCACGCCAGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGTGGCCCTGTGCAGGCTGAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGC
CTGTGCTCCAGGGGCGCGCTGGCTGGCTGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGTGGG
GCTGCAGAAGGACCTGCGTGCAGTGGGCCCCAAGATGGCCACAGGAGCACCCCTGGGCGCGTTACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCTGAGAATCTCATGAGCCAGCAGCC
ACCTGAGAAGCCTCTGCCAGCAGTCTGCGCTGACCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
GGTGAAGAGGTAGCTCCTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACCTG
CAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCCTGCAGGCGAGTGGAACTTCTTCCCCGAGTGGAGCT
TCGACCCACCCACTCCAGGAACCCAGGACCATTAAGATTTCTGAGGCTGGAGAACACTGCTTGGGCACACT
CTCCAGCTCAATAAACCATCAGTCCAGAAAGCAAGGTACACAGCCCTGACCTCCTCACCAGTGGAGGCTGG
GTAGTGCTGGCCATCCAAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGTTTCGACTGAGTCCACACTCC
CCTGCAGCCTGGCTGGCTGTGCAAAACCAATATTTTGGGGACCTTCTTCTGTTTCTTCCCACCTGTCTT
CTCCCTAGGTGTTTCTGAGCCCCCCCCCAATCCAGTGCTACACTGAGTCTGAGCTCAGAATCTGAC
AGCCTCTCCCCATTCTGTGTGTGTGTCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAGTAGAAGTCAA
AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGG
ATCACAGAGGCCAGAGGTCACACACCAGCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAA
TTAGTCTGGGCGTGGTGGTGTGATCCTGTAGGCCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
AGTTCAACACTGCAGTGAAGTATGGTGGCACCACCTGCATCCAGCTGGGTGACAGAGCAAGACCCTGTCTCTAA
AATAAATTTTAAAGGACTTAAAAAAGGACTTAAAAAAGGACTTAAAAAAGGACTTAAAAAAGGACTTAAAAAAGGACTT

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FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTPLLILLILLLLLPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ
ELLLELEKHNHRLAPGYIETHYGPDGQPVVLAPNHTDHCHYQGRVRGFPDSWVVLCTCSGMSGLITLSRNASYYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECRDLCFAHNCS
LRPGAQCAHGDCCVRCCLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWGDGACPTLEQQ
CQQLWGPGSHPAPEACFQVVSAGDAHNGCGQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRRCRKNAFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCSWGCRDRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSCLW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metalloproteases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

[illegible]

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FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYVSIACCQTS LCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

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FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTGTTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTAGTGC GTT
CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACTATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAAA

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FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

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FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCAATCAACCTCCTTCCCAGAACTAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
ACCGGGTTGGCGCTGCCCAGTGGAAACGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT
GTTGTTTCAGTGTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTGCTTCTTCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCTCCG
GGTCTACCGAGACCGATCCGACGCGTTTGGCCCGGTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAA
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGGCGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTACCGGACAGTTTCAGTTCGCCGATGGGAAACCCGGAGACCAAATCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTACACGCGGTACAGCCA
CAGGTGGAAAAGAACTTGGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
GCCCAGAAGCTTACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAGATAAAGTGAAGATTCATGGAATATTGTCCATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT
CGATTTTCCATTTTATGGCCACTTCTTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTCGATCCCAGTGTATCCAGAAA
TTCAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
TAACCTGGGAAGCTTCACATTCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTCC
TGTCTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCCGACTGTCCGATGCATTTGTCTGTGTTCA
CAGGATCCAACAAATTTCCCAATGTTGGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
AATTACCAACATTTCCGGCTGTGGAGATGACCCATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT
ATCTTCTCAGATTGGCTTCACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTCAGGGTCCTAACTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCCTCATCATTTGGAATCCTCATCCT
GGTCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCAGCAGATGGCCTGCGATGAAGTTTGAAGAGGCTCTGGACATCCTGCCTATGCTGA
AGTTGAACCAAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCATAAAATTTCTAGGACAGAACAACACC
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
AAAACATAAACTTATACAAGATACATTTACACTGAACATAGAATTCCCTAGTGGAAATGTCATCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGTTGCAAAG
GGATCAGAAAAAAAATCATAATAAGCTTTAGTTCATGAGG

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FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTOAFPHTEEVEVDSHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLRQCSSGFDHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTGVGATTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLKDNASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTG
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCTCTGTGTCATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTGAG
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGTCTCCATCCATG
TGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCTCTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTTCCAGAAATAATTTACATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTCTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTGCCAGAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTTAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTTGTCTCTAGAG
CTAAGACAGAAATTAACCCGTTTCAAGTCAAAAGCAGGGAATGGTTCATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTTCCT

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FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLQEKTFFTLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFAQKANCSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRD
SVQTCGPVRLLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

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FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGCA**TAG**ACCGCCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 476

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHRPSC
TTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTCAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTCTGTT
TCTTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCCGGTGAAGTGAAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAGGGT
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAAATGGATGATCCCTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCAGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAATACACGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCCCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCTTTTTTGTGCTCAGAAAATATTTCGAACGAC
CTTTCAAATCAATCCTTTTTCTGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATTTCTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTTTAGTGAAGTATTGGACACCAA
TGACAATCCCCCTGAATGATCGTATCATCTTTTCCAATCTGTTGCTGAGAATTTCTCTGAGACGCCGCTGGC
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCCTCACTGACTTGGGACACCCAGGCTGAAAACCGAGCACAAACATAACGGTCTGGT
CTCCGACGTCAATGACAACGCCCCGCCTTCACCCAAACCTCTACACCCTGTTCTGTCGCGGAGAACAACAGCCC
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCAGGTACCTACTCGCTGCT
GCCGCCCAAGACCCGACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT
CAGGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGCTGGGCGCCACAGACCCGCGCTCCCCCGCGCT
GAGCAGAGAGGCGCTGGTGGCGGTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGGCGGCGGAGCCGGGTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGACAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCGG
TGTGTGGCGCACAAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGACGCAAGCACAGGCTCGT
GGTGCTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCATTGCTCCTGGTGGACGGCTT
CTCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGGCCAGGCCAGGCCGAGGCCGACTTGCTCACCGTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCGGTGCTCCTGTTCTGTCGGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTCGGTGCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCCCTGTCCAGAGCTACCAATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAAGTGAAGT
CAAGTTCTTGAACCAAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT
CCGAAATAGCTTTGGATTAAATATTTCAGTAAAGTCTGTTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTTGCATTAAATAACAATGGGTTTAAATTAATGAGTATTTTTTT
CTAAATGATAGTGTTAAGGTTTTAATCTTTTCCAATGCCCAAGGAATTAATTACTATTATATCTCATACAGAA
ATCTGAGGTTTTGATTCATTTAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGTCTTA
TTTAAGAAGGCATATCTACATTTCCAACTCATTCTAATCTATATATTCTGTTTTGAAAACCATGTCAATTTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATAA
TCTGCCTGAAAATGAATAAAAAATAAACATTTGAAATGTGAAAAAATAAAAAAAAAAAAAA

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FIGURE 478

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQVFLFLFWGVSLAGSGFGGRYSVTEETEGKGSFVVNLAKDLGLAEGELAARG
 TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRI
 NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGDEGM
 IYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVLVDVNDNAPQFAQALYETQAP
 ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
 KINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
 GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPRLKTEHNITVLV
 SDVNDNAPAFQTSTYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHLPLASLV
 SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVDANDNSPFVLYPLQN
 GSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
 SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAEADLLTVYLV
 VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGFPFPGHLVDVRGAETLSQSYQYEV
 LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**ATG**GGACCTGTGCGGTTGG
GAATATTGCTTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCCAGCAAATGCCAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT
GTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCTGCTCCTAGAGATG
AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCCTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTCTATATCGCTATT
AAACTTTTTTCTTTTTTTCTA

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FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVLE
LGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMTATLKGL
VQKGVKVDLGIPLELWDEPSVEVITYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEGHVL
PAAETACLQETWTGKEITDGEKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:**Signal peptide:**

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

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FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCAACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTGCGGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCTACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTCAATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTTGGTCGGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAAGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTTCCATTTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACCTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

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FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQGPVTVNTSDFLVLD AQNYPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAACATTTCTGTTATC
TAAATAAACAGTGAAGTTTGTGTGACTAAAAAA

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FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

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FIGURE 487

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

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FIGURE 488

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSAFGEDGEEDDLWTVRCGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGATCACTGTGGTGCCCTTTTCTGTGCTGTGCTTCTGACTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGACAGACACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCCGGGGTCAACAGCCATGCAGTTCCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAACAACCTC
ATCTCTGCTGAATAACTACGTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAAGCCTGGAAGGCTACACCCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTACAGAGCAGCCCTCCCACTCTCAGGTGCTGTGCCGCTG
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCAAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCAGAGTCTGCTGCACCTTCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCCTCCGTGCTGCTCCTGAACATCGCCTT
CCTGCTGAGCCCCGATTGCAATGTCTCCTGTGCCCCGGGTGAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA
CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT
CCTCTCTGTCAAGAGCTCGGTATACGGACCTGCAACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTGCATGGGCTACGGCGGCCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCCTCACCGTGTGCTGCTGGGAACCACTGGGCCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCCAGCTGTTCCTCTTACCATCTTAAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGGTTCTGCTCCAGCGGTGCCGTGCAAGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGCCCTCAGCTC
CTCCCAAACAACACAGTAGTCCGGGCCCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACCTTTGTCTGGTACCTGGGCCCAGCTCGCCAGGGATGTGGGCAGAGCACC
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTACGCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGGAAGAGTGTGACGCTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGTAGGGGC
AGGATCTCATTACGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCCTTCCCAAAGATTGGGAGGTTCCGCCGTTCACAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTCTTGGGGGCA
GAGGAAAACGCTTCTTTCTCCTCCAGCTGAATCAGCTGGATCCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTCGAAGCTCAGGCCATAGTTTCAAGAAATCACCC
TTACCCACAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGCGGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
CAGCTGGAGGGGCGTAACCTGCAGGACTGCGCCTACTGAGTGACCAATTTCTCCAGGAGGAAAGGCAAGACAG
CTTACACGGCCATTGTCTCTTTTCCCAATGCGGCGGTGCACTTTCGCTCTTGGGGGCTGCACCCAGACATAGC
TGGCACCAGAGCAGGGTGTCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCCGTTTTGATGACCT
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAATAAATCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCCTCAGTTTTCC
TATTTGTAATAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAGAATTCAAATAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

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FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTLQNATTETWEELLSYMENMQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHAMQFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNI AFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSVKSSVYGPCPTIPVFDSEWNGTGQNMSCWVRSPVHSLVLMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

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FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTGCACACGGGCTGCCCTGAGAGACATTTT
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTGAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCTGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT
GGAGGTAGCCTCTCTTGTGTCAATTTCTTTTGAAAAATAACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAA

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FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMMDKGVLSYWRKPRNWLEVASLVSFSFEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGAGAAGTCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC
TTAGTGGCCGAAGCGGAGGGTGTGCTCAACCAAACAACCTCATTAATGCTGCAAACTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTTCGGACCTTCAGATTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTTAGTTACACCTGAACTGACCCTGTTTCAAAACAGGAATAGAAT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTGTAAAGAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
CAAGAAACAACAACAAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAAATGGATTCTCATT
CATACCCTTGTATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
AATGAAAACCAAATTTCCCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
TATCCTTTTCAAGAAATTTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCATTGTATAGTTATAT
CATTATTTAATTAATAAACAACCCTAATGATGGATATTTAGATTCTTTAAGTTTTGTTTTATTT
CTTTTAAGTTTTGTTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTTCATATATCTCT
TTGTTTTTGAAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCCTGCTTCTACAG
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAAATGGATTTATA

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FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAGAAQPNNSMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSC TKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTC
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIILTIIVGFIWLLKVNCGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVD TDLHTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

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FIGURE 495

CCAGGTGCACAGCGCATCGCCCCGAGGCTGTCACCGCCCTGCCCGCCCCACCCAGCTGTCCTG
GACCCAGGGGAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACCA**ATGGG**
GCTGTCCCGGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCCCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG
GATCGTGTTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCAGAGGCCAGCATCGGAAAACACCCACGTTCTTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTGCAGCAGTCACCAGGT
CCTGGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGAGGCCGAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCTCCACCCA
GATCACGTTCTGCTGCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTTCGCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGAGAGCCGCCCGGCTGCCCTGCTCCGTCACCCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCGCTGTATGAGTACCCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCCTCCTGCACGAGGGCTAC
GGGTTTCAGCGAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACT**TAGT**GGGAAGGCGGAGGT
GGGCCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTTGGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCTCCCGGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

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FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPPEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGOEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMI PADAP
AQWRAESYGVVWVAKVVFVVLALVAVVGAALVQLFWLQD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTTCGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCTCCACCTGAAATTCATTG
CTGGTTTCGGAGTGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
AGCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCCACGCGCTGCTGGTCTGGTGCAGAAGCACATTAAAGCTGTCT
TGAGTAACAAGCTGTGCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCCAGATCCGCTATTCCATGGTCAGTGTGC
CCACTGTCAACAGTGAATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
CCATCATCTGCCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGCCCTCAACCTGGACATCACAGGGCAGCTGAGGTTCGGATGACAACCTGCTGAACACCT
CTGCTCTGGGCCGGCTCATCCCGGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCCTGCGGC
TGCAGCCCTTCGTGGAGGTCCTGGCCACAGCCTCCAACCTCGGCTTTCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTTGAGATCTTT
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCTTGAGGCAAGACCACT
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCTTCCCTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTCCTCTGCCCCACCCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC

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FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPEPLELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIAVLNKLCLSSISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VNNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

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FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**GAAAGC
CCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCA~~AA~~ACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGCTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TG**AGACTCATT
CCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAA

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FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

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FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTACAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

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FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLQEGSQRRLLWRWCGSEEVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLI FLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

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FIGURE 503

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCAG
TCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACAA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTGAGGACCAGGGTCTGGACAGGCTTGGGAAGTGGTGGAATACTAGGATA
TTTGTTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
ATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTATATTGCAGTTTTTGAAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTAA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTTCGTTTCTAAGAGGTAAAGGTCAAATTTTCAAC
AAAAGTCTTTTAAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

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FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL
RGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKSSADSCNMSGITIVVLLGIAFVV
YKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGSG
SYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

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FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTCACCTTTTGAAGGACAAG**ATG**CATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCCACCGGCCAAAGAGGTCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCT**TGA**GAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCAATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGATGTTTCTGGAAGACACATC
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCAGGATCTAAAACTT
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAAA
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTTATTGTGGTAAAAACACATCACGTAAATG
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCCGGAACCTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACTCCTCTT
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTCTTGAGCATTGTATTCT
GGAAAAGTGTTTCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTATTTAACAAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYNNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDLOISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

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FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAAGGCCAGCTTGTTATTAAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA
GACCCTCTTGGAACCTTGCCAGAGCAGACCTCCCTGAACACTTGAAAGCCAAGACCTGTGCG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGTGGGCCACACCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTCAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTTAAAGAGTGTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTTCAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTGTTTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAAACCTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACCTTTTTGATGGTGGCCCTGAACCT
CATCTGCTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCCTGGAGGTCCCTGGTTCGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATTCTTGAATTCCTT
GGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

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FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTTEECMDKMMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVLIKETAFDILQYSEPSRFRWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLKLKLVKEGVVKDLSSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

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FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCTTCCGCTCCAACATGG
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTCCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCTGTCAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTAAAATTTACA
TACAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGACACATCTGT
GTAATAAACCCCAATAAAATTGCCATCACCTCAG

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FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAASYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

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FIGURE 511

CAGCCGGGGCGATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCGAGCCCCGTTCCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCGAGGAGAGAGGAGCCTGTCAACCCTGTGGAGAATGCACTCCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCCGACACTGCTAGTGGCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCTCCTGCCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTTAAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCACTGGACGCTTCCCTCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTTTAAATTAATAATCATGTTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTGAGGGAGGGC
GAACTCGATCTCAGAGTTTTTATTTTATTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAAATGGCATATTTTAAATTTGGCCAGACCAGAACCCAGTTTCTCCTGTTGGGATTAT
TTGTTAGTAATCGTTTTTACAGGCTGAGCATTAACTCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAAATAATGCTGTAATTTCAACTTCAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAATATTTAAATACTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTAATAAATAAACTGTACAAAAATATAGATTTTCCCTATCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCACTGTTTTGGGGATTCCAGTAATTAATAATCTCTAGTGAACAAA
GACCTGTTTCAAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCCTTGTTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTTACATACAAGAGGTGTTGCGTTTCATTTTGGGGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCCAGCTGTTGGACCTGC
TGCTTTAGAACCACAGATTGGTACCTCGTGCC

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FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCACTGCTCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCTGTTCGGGCCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTCAGCCCATCCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCCTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCTCCAGCTCAGCCACTGCAC
TGAGAACATGGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTCACCGGGGATGCACGGTCTGCATTTTCGGCCCCCTGCGGGACAA
TGGAGGCCTCTCTCCCTTTGTGCCCGGGCCCCGGGCCCTCTGCAGACAGACCTCCATGCCCA
GAGGTGAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCAGCTGCCAGCTGACCCCTCAGTTCTCTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCCCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCCAG
TACACACAAGTTTTCCCTGCTGCCACGCGAGGGGAGCCCTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
CCAGCGCATCAACAGTGCAGTGCAGGTTGAGGACAAGGCCATCTCGGAGCTGCAGACCCCTC
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGGCTT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
TTCCCAGGACTCAGCCCAGGTACCTCGCTGATTCTGCCCCCTTCCCAGCTGCAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTCAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAAATGCCATCTCGAGCCCCTACAGCTC
TACGGGAGGCCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCAGTCCAGCTG
ACCCCTCAGTTCCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTTCCCTGCTGCCACGCAGG
CGAGGGGAGCCCTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCAGTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

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FIGURE 514

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
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VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTS LI PAFPPAASMDA
GMRRTRHGTSAPAAAAAAPRSTLNP TLGSLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

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FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGCAGCGGCCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGAGCCATCTGAAATGGTCATGAACCCCAAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAGTAAGTTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCACCCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTACAAAGGAGGGGAT
CAAGCTTTAAGTAAGTCCACAGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTACCCCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAACTGAGGAGACCCAAGAGAAACGAAGGTCTTTC
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACAAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAAAGAATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
TCCCACAATGCTGTCCACTACGGGAAGCATTGGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATACCCGCTTAAATACTTACACCAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAAATGCCTGTGAAGAAGCATTAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
TGGGAAAAGGTCAGCAAACTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACTCTTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTTATTACTTGGACTAT
TTAATGTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTCAATTTCTAAAACCCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTAGCAGTCTGTGGCATATTAA
TCAAACCTGTTGAATTGTTTTCTTACACCCTGGAAATCTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

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FIGURE 516

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKFHMPEDVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKRQGAQTVFNKFSNMNWPVDIHPLNKSLVKDNKWKKTETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIYVEDKHKILYCEVPKAGCSNWKRILMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSCLCPC
LINYDFVGKFETLEEDANYFLQMGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTPLL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

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FIGURE 517

GGAACTTCCCAGGCACCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCAATGCCTCTGTCCAGCCACCTGCTGC
CCGCCTTGGTCTCTTCTTGGCAGGGTCTCAGGCTGGGCCTGGGTCCCCAACCACTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACCACGGGGCCTCGCCCA
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCTGGGCCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCTGC
GAGAGGCAGCCTCCTCTTGAAGCTGAGGCTCTGGTACCACGCGGCCTCTGGAGATGTGGCTGAACCTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGGCCGATCCGGGGTGAATTCGAGTGACCTTCTTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCCACCCCCAGGCCAAGTGTCCCCGGGACACC
ACCACTGCCGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAAGTGTGGGGGACCTGTCTG
ATGAGAACCCTACTCAGCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGGAACCACCGTGTGGTGGTCTGAGCGCCCTCCTGGCCACGCGCTGACCAAGCCGGAACA
GTGCACAGGGTCTCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCTGCTATACTCTCAGCCCCGAATTCCAAG
CCTCAGGCACCTCCAAGTGTCTGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCGGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCTGGCCGGGCGAGACAGGCCCGG
GGGGCGTCTGGGTCTGGACGACCTCATCTGTCTGACCACTGCAGACCAAGTCTCGGAGGTGTCCACCCTGCAGC
CGCTGCCTCCTGGGCCCCGGGCCCCAGCCCCCAGCCCCCTGCCGCCAGCTCGCGGCTCCAGGATTCTGCAAGC
AGGGGCATCTTGCTGCGGGGACCTGTGTGTGCCCCGGAACAAGTGTGTGACTTCGAGGAGCAGTGCAGAGGGG
GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
GGCGGCTGCAGTGGCGGCGTGTCTCAGCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCTGT
CTCTGCAGCGGGCCTGGGGGCGAGCTAGGCGCTGAGGCCCGGGTCTCACACCCCTCTTGCCCTTCTGGCCCCA
GCTGTGAACCTCACTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACTGGCGTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGGCCACCTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
CTCTGCCCTAGCCATGAGACGGGAAGGGGAGGAGACACACTGTGGTGCGGGTGAGGCACCCAGGGCAACCGCT
GGCAGGAGGCTGGGCCACCCCTTTCCACACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTCCGAGGGCCCTC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGTGGCGCCGGGCCCTGCTGGGCCCCTAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCCTGGAGGCCAAGGTCTCTGGAGGCGGCAGGCCAATGCCTCGG
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCACTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGCGAGCCAGGCACCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGGCCACGGCGGGCTTGCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGGAG
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCGCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTTGTGCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC
CCGGCCTGGGCGGATACAGTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCCAGCCCCCTGTGGACC
ACACCTGGGACAGAGGCAGGCCACTTTGCCCTTTTGAACCTGGCGTGTGGGCCCCGGGGCCGGGCCGCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCAATGGGTTTTCTGAGC
ACTTCTACAAGGGGGAGCTGAAGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGCGGCACCAAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCAGATCGTGTGTAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
AGCCTGCCCCCAGCCCGGGGAACACAGCCGACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC
TCATGCTCCTGGTGTCTGGGACTTGGGGGACGCGCTGGCTGCAGAAGAGGGGAGCTGCCCTTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGTGACATCCAGCACTTGGTCAGACCCTAGCC
AGGGACCGGACACCTGCCCCGCCCAGGCTGGGACAGGTGCAGGTCTCAGGATATGCTGAGGCCTGGGCGTCCC
TGCCCTGTGCTGACTCTGTGCTCTGTGAATAAACACCTGGCCCATGAGGGCCGCCCCAAAAA

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FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDSDEAQCQGYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETTLTWQSTGPGWPGW
QELAVTTGRIRGDFRVTFSATRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGSNRHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPTGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPAPAPQPLPPSSRLQDSCKQGHACGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCELHLAYYLQSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPDIGTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAGWPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAERAWRVVFEAVAAGVAHSYVALDDLLLDGQPCPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPQPPVDHTLGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKELKVLHSAQQQLAVWGAGGHRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQPPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGRRWLQKKGSCPFQSNTEATAPGFDNILFNADGVTLFASVTSDF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077

Amidation site:

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

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FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACATATCAGCTCCTGGCATCTGTAAGG**ATGCT**
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAACACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTCTATAGAT**TGAG**ACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

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FIGURE 520

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
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HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQOGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

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FIGURE 521

GATCAGTGTGTGAGGGAAGTCCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA
TAAGAGGAAGTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCAGCTCCACTTTCTCTATG
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCATGCTTTTCAGTTT
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCAAC
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTCTCTCTGGGCTCACTGTTTCAAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAAATGATCTTCTTGGTTCATCCCAAAACCA
AAGCTTTTACTCACTCATGGTGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA
TTGGGTTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAT
TTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAGAAAGACCTGATGGGGTAATCCTG
TTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCTGTTGATTTTCTTAGGTGTCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC
ATGGATATAAAGAGGTAAAAAACTTAAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
CTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAGGTGAACAGATATTTTTGGGATTAGTAACATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATCTTTAAAAATGATGAATACTCATAATTCTTATCTC
TATAATCAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAAGTGCCTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAATATTTTGATATGTAAGCTCTACACAAAGCTAAATATAGTGTAAATA
ATGTTTACACTAGTAAGCAAATATGTTAATCTTCTATTTTTTACTGTGATATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTGAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAATAAATATAAGTATTTTCTGTGTATGTATACA
ATAAATATAAATAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

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FIGURE 522

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLLQLFCVCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
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LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPVMGVPIFGDQLDNIAHMKAKGAHAVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAHD
LTWFQHSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

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FIGURE 523

GGCTGCGGGGTCGGCACGGAAGATGCACGCGAGGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCTCCTGCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAAGTGGAGGGCTCCCCA
CCGAGGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGCGGCCCTTCGACTCTTGGAGGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCCCTGTTTTCTGGTCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTG
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGGC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCCTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAACA
TCACAGACCCCAACCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTTGCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAATGTCA

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FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLWLWGLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSLOKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQASWTSLOTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGLRKSCGIAGGDKTERRDSPRATDLAGKRTES
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTVQVAVEDSFLSHHHWLWVKLALKTG NVSKI
NAAFQDNPAFCPPAWGLSQQDYLRKALSAQQELPSSSRDPSTLENSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAQGEQTPKEGADAVSGTQKGKGQGGQGGQGGQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKREL SHHAAGVGVVSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

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FIGURE 525A

AGTGCCCTCTGTCAATTTAATCTCCACGGAGTCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTCTGTAAAGACTGTCCTTGGGTCATTATGTGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGCACACGTGTGTGTTTGCCTGTACATGTGCATGTGTGTG
TTGTGTGCCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG
TGCTTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAAAACATTACGTTAATAATCACAAAGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGACACAGGGAACCTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCCTCCAACGGCCACTTGCTG
AGCCCGTGCTTATCTGTTCAGTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
ACTCTGTGCCAGCTTGGTGCAAGGCCCTTGTGTGTGCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCACTTTGAAGATGAGGAGAGCACAATTCTAGATGGAAATGGAGGTACGCGAGTGGAAA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCTTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
TTCCTGGTTGATTCTCCCCACTTCCCCACCCAGATATATCCCATCGCTGCTTGGTGGACAGTACGCTGCTG
GGTTTTGGTAAAGGTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAATGGGGC
CCCATGAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTGCACTACCTTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTCCCTTGCTGAAAGAGAGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTTAAAGTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCCTT
GAAATACACGAGCAGCTAAACATAATCTTTCGCTTCCGTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAAACAAAGGAACACCCAGCTGTGAGAAGTGGCTTCTCAGCATTCTGTCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCCATCAGGGTCTGATGGTTGCCCTGTTTCCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTGTCTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCTGACTTGAGCAGACTGATATAAGTGAATGCAACATATTTAGATGGCACAACCTAATTTAGATTT
ATCAGTGCTAATATAGAAAAGCTAGTATTTTATGGGGCTTATTAGATTTTATGCTGAATCCTCACAACTTACG
AGGGGGTTCGTTTTACAGACTATGATCTGTCATGATTTCCCAAGATGCTCATTAAGTATATGGTGAAGTAGA
ATTTGAATACAGAGACCTGGTTCTGCTACTTCTGTGTTTCTATTGGTTCAAACAGCCTTTCTTCTTTCAA
ACAACCTCAGTGCAATTCATGGTTTTGGAAAATAAACTTGATTTTGAGATTCAGACAATAAGTGCATTTTTAATG
TTTATCTTTTATCTTGAAAACCTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
CACAGACAGTACAATGACAAATTGGAGATCAGCTCTAATCTCGGCCCAATTTAATGCATTGCTGAATATTCTT
CTGAACATAGTCCATCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGACTTCTGCAG
TCAAGAGAGCTGGGAACTCTTGGACAGTCACAATGTGCATTTGGGTATTAAGGCTCTGCAAGTTCTGCACCA
AATAACCCCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGCATTCATCCAGCA
GGTATTTACCAAGCAGGACTTGGGCCAGGTCGCTAGGCTCTGCAGGTGGACAGCCAGCCCTGACCTCCA
TGGTGTCTCTCTCATGGGAGAGGCTGCACAGCAGTCACTGAGAAAACGAAGAAACACAGGTAATTTAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT
ACATACAAATAAGATACATGTGTATAATTTTATGTAATTGACATCATTATATGCTGGACCTGCCTTTTTTG
CTTAATGAAAATGTCAAAGTAAATATTACCAATCAATCAATATATTTACCATCGTGTTAATTTCTGCAGAGCA
CTTATTCAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCACTTCTGAAATGATCTCCTTAGAATAAATTCCTCAATTTGATTGCTGGGTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCCATTTTCTAAATGCTTACTATGACTGGTTTTCAACTACATTTTAATTCTTGTTCAATCTGATAGGCAAA
AAATGATATTTAATTTTTATTTGATTGATAATGACCTTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT
GAAACATCTGTTCTATCCTTCGTCAATGTTCCCTTCAATGTTAACTTTTCTTATTGATTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTGAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGTCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCAACTTATGATTACATAAATATCTCCCATATTTGCTCTTAGCATTTTTTTTC
TTTTCATGTAACCTTTGTTCTTTTCAGGAATTTACTTTGCGGTGAGAAATGGGCTGGCTTCCAGTTTTATGTTTC
CCAAATGGTGATTGCTGCTTCCATATCTCAGTCACTCTTTGAGCTATCTTTGATTCTTTTTCAAACCAC
TCTGCGTACTTGTGCTCCCTTCTATAATCTCAGTCACTCTTTGAGCTATCTTTGATTCTTTTTCAAACCAC
ACTGCTTTACTGAACTGTCACTCATCTTATACATTTTTAATACTCAGCAAGACAAGTTTCTCAATGCCACTTTTT
TCAGAGTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAATCACTCTTTTTGTCCAAGGTA
AAATATATCCACATTGAGATCACTGAATATACAGACTAATTCAAGAAAAATGTATGCTTTTATTGCATTGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATTTCACTGAGACTTATTTTTGGCTTTTTCA

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FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTTAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTTAATAGTTTTCTATTATTTTGGGTTTTCCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTCCAATGTTTCATAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

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FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLP LLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRLCLGLPREVVT LRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

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FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAACTTAATCCTGATCCA
TGTAACCTTTGGCATTTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTGTCTTCATTCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTACAATATTGAAAATAGGAAATTAGTTTGTAAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTGA AAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

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FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYYFK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

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FIGURE 529

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAAACATGTCA
AAGTTAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAAACTATGGGGTCCATCTTCGGCTGTGAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCCTACAACACTGAATGGAGGTCAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAACCCAGTGCCATGGCAGTGGAGTCATTTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTCGCCGTGGAGACTTTTTCTAC
CACAGCGAAAATCCAAGTATCCAGAGGTGGGAGACTTGCCTGTCTCCTTTCTATGCTGGA
CTGAGCGGGGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAATAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTTCTGTCTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGGCCTCCTCATTGCCGGCCTGGCCCTTGTGCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCACGCCTGCCTGGCTGCTTTACCTGGGAGTGCTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTCAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTCATAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGGAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAAGTTTGTAAATAATTTCTAAATTATCA

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FIGURE 530

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKLRRHVE
MYQWVETEEsREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFAFVCVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE
```

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

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FIGURE 531

AAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTTCCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACTGCCTGGCTATTTTCTCAGA
TAAGACTTCACTGAGTGACTGTTTCAAGCCATGATTACCTGCAGTTTAAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTCATTATTACATCCCCCGCCTGTAGCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

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FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGSGIRSHQLSAGHLGL

Important features of the protein:**Signal peptide:**

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

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FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCGGGGTCTGCAGGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
TAGTCCCCATCCTGGAGGGGACAGGCTCTGCGCATCTGCTCCTGGC**ATGG**CGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACACGACAGGGCAGACCCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC
GAGGACAGACGACGCGCCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC
AGCACAAAGTGTTGGCATCGCCCCGCGCCCGGGACAGTCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCACAGCGGGCAGGACTCCTCCAGCACACCACACCCAGTGGCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTTCATTGTGCAGAAAAGTCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCACGTGGGGCAGGCCACATCTAACCCCAACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTCTGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 534

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEEAAMI PPPQSSDVGSAGKEDPPRQ
GRPPI PAPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGGAGCGCC**ATGG**
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTTGCTACTAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTTCTCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCCACCAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTTCGAGTTG
TGTCCTCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTTTAAATGTTGTCTCTCTGTTTTCATCAGTTTTTGTTT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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FIGURE 536

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLFLLVVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

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FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACTCCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAAGTTGAGACTTGTCAAGAGGCTCTATTTTGGGTGAGGGTCCTTCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGAAAAAGAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAAGTTTCTTATGTCCCATGGATCTCTCCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

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FIGURE 538

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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FIGURE 539

CGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

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FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRODYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

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FIGURE 541

CTCCACGAGGCTGCCGGCTTAGGACCCCCAGCTCCGACATGTCGCCCTCTGGTCGCCTGTGTC
TTCTCACCATCGTTGGCCTGATTCTCCCCACCAGAGGACAGACGTTGAAAGATACCACGTCCA
GTTCTTCAGCAGACTCAACTATCATGGACATTGAGGTCCCGACACGAGCCCCAGATGCAGTCT
ACACAGAACTCCAGCCCACCTCTCCAACCCCAACCTGGCCTGCTGATGAAACACCACAACCCC
AGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACA
AGAGCACCAAAGCAGCTCATCCCCTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAA
GCACAGACGTCCAGACAGACCCCCAGACCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCT
TCTTCTATGATGAACACACCCTCCGGAAACGGGGGCTGTTGGTCGCAGCTGTGCTGTTTCATCA
CAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGGTTATGCCGGAATCGTT
GCAGGTGAGTCCATCAGAAACAGGAGCTGACAACCTGCTGGGCACCCGAAGACCAAGCCCCCT
GCCAGCTCACCGTGCCCAGCCTCCTGCATCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACAC
AGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCCTGCCCCGCC
CTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAG
TAAAGCACTGTGGTCTTTAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 542

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLEGTDGPLVTDPEETHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTS GKCRQLSRLCRNRCR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

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FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTCAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC
GCTCCGCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGGTTCTGGCAGAAGGGACGCTATGA
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCCTGAAGTGTGAGGCTCATTCACAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAGGGTATCTCTCTCGACGGCAGACCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGTAGCAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

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FIGURE 544

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCQAHSQNVTFVL
RKVNDSGYKQEQSSAENAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFSLVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

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FIGURE 545

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGG
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCCAAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACCTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAACTCGTTTAC
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTTAACCCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

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FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81; NX(S/T): 2
MMLIPMASVMAVTEPKWVSWSRFLWVTLLSMVLGSLALLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSQVKKVMSIPKGNLSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRTTQVLVGHHPHPQDVEKQMQEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQQRSDYYHVLEAANEGDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

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FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTCTAGTCCAGGGTGTC
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAAGTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCC
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCAGCCCGGCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCCTGATGGGTCCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTGGCAGGGGGACAGGAGACTGTAACAGGCCCCAGGTCCTTGTCAGCCCCCTGAATGC
ACGCCCCGCTTCGGTCTGTTCCCTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCCACCATGCGG
GCCTCAGGTGGCAGAGAGGCCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAGGCAGGCCCAGCCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCACCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCCCCTTCCCCAACT
ATGCATTCAATCAGCAATAAATGAGCCTTTGCTGCA

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FIGURE 548

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAQPTDSGT
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPNTAGILAATTIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGHDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCQLVPTS

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTCACCACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTGTT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCCTGGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCTGGA
GAAGCGGGGTGGGGCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAG
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACGCCATTTGAACCTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTGCTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACACCTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTGTCATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGCTGTGGTATCATGTCAGCA
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGACAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTC
CTGTATAGTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCTCGCAGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAAGGAGAGCTCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCGTTACAGTGGAGCGTTCGTGTCCATAAAACGTTTTCTAACTG
GGAA

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FIGURE 550

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSP TARAGPGQAWSLRC
VLVGILHSDRRCALPTFP HSSFACGAHPFAESSFPCGLWPAEVK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

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FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCCTGGTGAGGCCATCATGCTGGCCAT
GACCCTGGCCCTGGGTACCTTGCCTGCCTTCTACCTGTGAGCTCCAGCCCCAGGCCCTGGTGAAGTGAAGTGA
GCTGTTCTTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCTTGTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCCGCGGTTGGCCTCAGCCCCATGCACCTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCACCCCTGGAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGCGCTGCATGCCCTGCGCTTCT
ATTCATGGACGGCAACTGTTATTACAAGAACCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCGCGCTGCGACCAGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCTCTACAA
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTTCCGGAGCCTGGTTCGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTCCGCTCACTCGATGAGACCAGCTCCGGCCACTGGCCCGCTGCCCATGCTCCAGACTCTGCG
TCTGCAGATGAACCTTCAACAACAGGCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTCGGACAACCGCATCAGCGGAGCTTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGTCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA
CCTGCAGTGCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCACTCAATGGCTCCAGTTCTGCGCCTGACCGG
TCTCAGGTGCTAGACCTGTCCACAATAAGCTGGACCTTACACAGAGCACTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGAGGGCGTGGGGCCACAACCTTCAGCTTCTGTCG
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG
TACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCGCCTGCACACCCTCCTGCCCAAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCTTGCCCAAACCTGGAAGTCTCGACCTGGCAGGAAACAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCTGTCGCCCCGGCTTCTTTT
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGCCCTGCAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
CTTCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGGCCAGCTCCA
GGGCCTCAGCATCTTTGACAGGACCTGCGCCTCTGCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCCCTC
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGA
GTGCCGTGGGCGCTGGGCACTCCGCCTGTGCTGGAGGAACCGGACTGGCTGCCCTGGCAAAACCCCTCTTTGAGAA
CCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGTGAGTGGTCTCTT
GCGCGCCAGCTTCTGTGTCGCCCCAGCAGCGCCTGTGGAGGACCGCAAGGACGTCGTGGTGTGCTGATCCTGAG
CCCTGACGGCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTTCTGCCCGCAGAGTGTCTCTCTGTCGCCCCA
CCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAA
CCGGAACCTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

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FIGURE 552

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELPQPHGLVNCNWLFLKSVPFHFSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPVGLSPMHFPCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYY
KNPCRQALEVAPGALLGLGSLTHLSLKYNNTLVVPRNLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTSFSLSRLEGLVLKDSLSLWLN
ASWFRGLGNLRVLDLSENFLYKCIKTKALQGLTQLRKLNLSFNYQKRVSAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLALDLSYNSQPFQGMQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRLHTLLPQTLRNLPKSLQVLR
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDHWSWFGPLASALQILDVSANPLHCACGAAFMDFLELVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMHLHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016**Amidation site:**

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

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FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTTCGGACACTTCAAGTTCTGC
ATTACTTTATTTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAACTGGCACAACGTCCTTAATTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVFTNLSLQNTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFPEPVFEGGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTTTTCTGGAACCACTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGAAGTCTAATCCAGGTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAAGATGCACC
TACTGCCCTCACCACCTGAACCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGTCAGCGGAGTTCACCCGTGTGGGTTCCTG
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAACTGAGCCAGTTGGTGGGCGACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGCACCCCCGTGCCCCCTCCGCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
CCTACCCTTGCCCTTGCGGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTGCGCGCCGTGGGCAACTGTTGGTTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCCTCTGCACTTCAG
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGACAGGACAGTCCTTCCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCGGGCACCAAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCACCCCTGTCTTGAGCCCGTCTACCAAAATAAAGTTGTAG
TGATTCCA

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FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLI DSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

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FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTGAGCATTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTTGACCCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTGACCATTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCCTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTCCTTGTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

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FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

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FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCGCCCCACGCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCCTGCGG
AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGGCTCACGCGGCTGCGGGTCCTCAACGTGAGCTACAACGTCTGGAGTGG
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCCTGGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC
GGCTTCCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTGCGGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTTTCAAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCATTGCCAGACTGCCCATTTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTGCCCCCATGTTACA
GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCAAGGTTTGGGGG
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCTG
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCACCCCCACCCCG
CCCCACCACCGCCCAAGTTCTTTTCCATCATTTATAATTATCCTTATTATCTTGGTAAAAT
ATTTATTAAGTGACTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
AAAAAAAAAAAAA

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FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTIVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAAALHALPGLRRDLDSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG
ERLRELDLQARNYIFEIEGGAFDGLAELRHLNLAFNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETDLDSHNQLLFFPLLPQYSKLRTLTLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTVSLWEEFSSSDLADLRFLDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVP
LFANARNITTLDMSHNQISLCPLPAASDRVGPSCVDFRNMASLRSLSLEGCGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIIPSC
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSV

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

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FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAGT
TTGGGCTGGAAGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAAGTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCC
AAACAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLWVPGQSDLHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDVPV
EPEAFRAEDSEGEAFSESTEGLOGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGESERTGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYK
DCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

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FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTCAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

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FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

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FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCAATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTGCGGGACCTGGGTTCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

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FIGURE 566

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

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FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCAATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAGTGAACCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

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FIGURE 569

GGTGCCAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTGTCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCCTATTTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAAGAAAGAGACCGAAAGCAAAAGTCATAAACC
ATGCCCCACGAGCTCAGCTGTCCTGCTCCGTGTCTCTCCATAACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGTCTTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC
TGTCTACTTCCTGATCCTCTCTTCTGTGCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCCTCTGGCTCCCAAACTGCCACTGTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTTCCAAAATAAAAGAGAATCTTTCTTCCCTAAAAA

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FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLGRQYVNEVFNFSDKLYDLLFTNSPFQRFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDYFRHLESELAKTESTYLAEMHRQ
SPKEKASKTTTVRRRKRPAAHLRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

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FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTTCCCCTGTGGATAAGGGTGGACGGCTGCTCTGCAACTT
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGCAGAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTCACAGA
GGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCTCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCCTCCACGTGGTGAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGCTTGTGCCAATAAAGGGAGGTTGAAGTCCGATCCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAGAACAGATCCAGGGATGGCACAAGGACAGCTG
CCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTTCAACAGAGAGAAGCT
CAGGAGGCAGCGGACAGGGCAGCCAGCTCTTGGACACCCGACAGCCGAGGGGGAGGCCAGGCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGGCCACACTTGTG
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCCTGGTCCCATCTCCAT
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGAGAAACCAATTAGGTAGGAAACATGAAAAACCTTTGA
TATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAAGCAATCAA
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCCCTTCTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTTCTCTGGCAGGCCACAGTCCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTTAGCAGTCCCT
CACCACCACATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAAATCAGCACCCCATCCAAGTGGCCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTCAGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTACACAAAAAGCAAACCTACATTTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAAGTGAAGA
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTGAGAATCCAGCCCTGCTGGCTACTAAC
TAACTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATAATCGTCATCATTTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTCT
TGTGCAACAAACCTGTTTAGGATTCTTCCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCT
TGAAGTTCGACTGTGTTTTTATTTTTTTCATCCAACCTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTGATCTCTTAGATTTCTTAAAGACATTTTAATGTATGGTTAGGTTTTATTTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTCTTCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGACACTTTTTCTTACTTTCATGTCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTTGGGCTGAGTTCACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTCTGTTCAAGTTGGCATTCTTGTGTTG
GAATAAACTATTTCTTGG

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FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGRLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGTDKSCPLNGH
LQHCLETVREEFII FNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

FIGURE 573

CTCCAGTTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAATAAATAAAACGCTC
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGCCGAGAGG
AGACCTCAGCATCATCTAGAGCCAGCGCTGGCCCTGCCTCCGCCTGCGCCGCCGCCGCCGCTGCCGTTTCTGTT
CCTGCTACTGTCCCACCTAAACAACCTCCCCTTACACGGACAAGTGAACATCTGTGGCTGTCTCTCTCTTTCTTC
CTCCTCTTCCAACCTCTTCTCTCTCTCCACTTCCCAGCCGCAGCAGAAAGCCCCCAACCCAACCTGACGCTGGCA
CAACTGCAACCGGTGCATCCGACAACACTTTATCTCGCTCCTCGGGCTCCCCTAAGGCATTGGACCCATCGCCGC
GTCTTTTATTTTTGCAAAAGTTGCATCGCTGTACATATTTTTGTCCCCGCCACCTCCTCTGTCTCTGAGGTGCC
TACAGCCCCGCAAACTCCTCCTGGAGCTGCGCCCTAGTGCCCTGCTGGGCAGTGGCGTTCCCCCCCATCCTCCC
GCGCCAGCCCTGTGCTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCGAAGCGCTGAAAAGGAGAGACAGGAGGATGATGCTCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGTGGCTTCTACCTCGGCTGCTCGCTGCTCGGAGTGCAGAGCCCGGGCTAGGGCGCCTG
GAGAATAAGATATTTTCTGTTACCAACAACAGAAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCACTTTGCT
TCTCCACATTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGGAAAAGACCTAGTACTTCTCTGCTC
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAACCTGCGGAT
GAGTTTTGCTTTTTACTATGCAAGAAAAGATGCTGGGTTGTGCTTTCCAGATTTTCCAAGAAAACAGTCAAGAGGA
CCAGCATCTAACTACTTGGACAGATGGAAGAATATGACAAGTGGAAAGAGATCAGCAGAAGACCAAAACACAAC
TGCTCTGTATTACAGAGGTTGTGAGTGGGCTGCGGCAGCCGCTTGGTGCCCTGCATAGTGGGATGGCTCGCAAC
CGTCTCTTCATTCTGGA AAAAGAAGGTTATGTGAAGATACTTACCCTGAAGGAGAAATTTTCAAGGAGCCTTAT
TTGGACATTCAACAACCTGTTCAAAGTGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCCAT
CCCAATTACAAGAAAAATGGAAGATTGTATGTGCTCTATACCACCAACCAAGAACGGTGGGCTATCGGGCCTCAT
GACCACATTCTTAGGGTTGTGGAATACACAGTATCCAGAAAAATCCACCAAGTTGATTGTAGAACACGCCATA
GTCTTCTTGAAGTTGAGAATCCACAGAAGACATGCGGAGGACACTGCTTTTGGCCCTGACGGCTTTTGT
TACATCATTTCTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTTAAGTGATTTACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATCCATACCAAGGAGCAACCCACACTTC
AACAGCACCACAGCCCGCCGAAGTGTGCTCATGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCACTGATATAAACATCAATTTAACGATACTGTGTTCCAGACTCCAATTGGA AAAACAGATCATCAGCCAGAATT
CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTGAATTTCAAGCCATTAGTAATGGTCCT
TTGGTTGGTGGAATTTGTATACCGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTTA CTCTCCAGCAAAGTCTGTGACAAAGCAGTGGCAAGAAAAACCACTCTGTCTCGGCACATAGT
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTGTGGAGAAGATGAACTAGGTGAAGTTTACATTTTA
TCAAGCAGTAAAAGTATGACCCAGACTCACATGGA AAACCTACAAAATTGTAGATCCCAAAAGACCTTAAATG
CCTGAGGAATGCAGAGCCACGGTACAACCTGCACAGACACTGACTTCCAGAGTGCTCCAGGCTCTGTGCAAAACGGC
TACTGCACCCCGACGGGAAGTGTCTGCTGACCTCAGGCTGGGAGGGGACTTCTGCAGACTGCAAAATGCTGAG
CCAGCATGTGCTCATGGAGGTGTCTGTGTAGACCGAACAAGTGCCCTCTGTAAAAAAGGATATCTTGGTCTCAA
TGTGAACAAGTGGACAGAAACATCCGCAGAGTGACCAGGGCAGGTATTCTTGATCAGATCATTGACATGACATCT
TACTTGTCTGGATCTAACAGTTACATTGTATAGTCTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT
TTTTTATCCTGTCTATTAAAAAAGACTGTTATCCTGCTACACACTCCTGTGATTTCATTCTCTTTTATTAA
TTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGATGCTCAGCATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTGCATAACAGATGATTTTTTAAAAATATACTTCTTATGCAAAAGTATC
TTACACAGAAATTCATGTAAATTGTAATGGAATTTTTTATTGTTACTAGAAGATTATTTGACTTCCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCAACTTTAATAGAGTTTTGAAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAAGGCAATATTTTATATTAAAGTACTATACTAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATTTGAATCTTCATTTTTTGTCAAGTGTATCCAGTTACAGAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTCATCTTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT
AATAGCATATTTTAAAAACAAAAA

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FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVRSCSRQRRPQHHLEPSAGPASACAAA AVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLPLPSRSRKPPQTQLT LAQLQTVSSAQLYLAPRAPLRHWTH
RRVFFYCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLL GSGVPPHPPAPSPCCSG
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTECGKLL EEIKCALCSPH
SQSLFHSPEREVLERDLVLP LLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGG L
CFPDFPRKQVRGPASNYLDQME EYDKVEEISRKHKHCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKN GK
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARV FLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLR LDVDTMCNVPYSIPRSNPHFNST
NQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNR SSARILQIIKGKDYESE P
SLLEFKPFSSNGPLVGGFVYRGCSERLYGSYVFGDRNGNFLT LQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLY KIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTAKCE PACRHGGVCVRPNKCLCK
KGYLG PQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

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FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCTT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGACCTGCAGTTCTGCCCACACA
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATT
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGACAGAAGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCGCAAGCAACAAC
TGATCATCCGCGGGGATGCTGCCACAAGGAATAATTGAGCACTCATTGACAGACAGGGGAAACC
ACTGCCTCTTTTCACTCTTTCTCCAGATTCCAACAGTCAGTGTTACAGCATTTCACCTTGTTC
ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCACATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
CCGCTCTTCCTTTAGTTTCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTAGTTTCTTGATAACCGTCTGGGAGGATTG
CTGGCTGGTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTTCAAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
TTCACTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGCAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCAATA
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTG
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA
CCCATTCTGCTCTCCTCTTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCTT
GAGATAAGGAGGAACGTCTCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTTGAGCCTTGGGGGACCAGTTTACCCTACATCCCAGGCTTCTGTTGTCCCTTGCCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTTRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

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FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTCTATTTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTTGAAGAGGTACGCAGGAAGTATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATTAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTCCATCTTTGATTCACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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FIGURE 578

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

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FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTCACAGTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTTGAAACAGCCATTTCTTCTTTTTGGCAAACTGAAGAGGGTTTAC
ACAACTTATTTTAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCATTTCTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

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FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNEPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

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FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCCAG
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCAATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACATGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGATGTCAGATTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGTATGACTGCCTTTG

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FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELESLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLETFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

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FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTTCGACGCGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCCTCCTCTTCTGCTTCAGAGGGAGAGCAGGCCCCGTGCGCCCATTTCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCACTGGACTAAGAGTGGG
CTGGCCCTAGGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAAGGTACACAAGCAGGCCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT
CTGGTTGCTGGAGTTCTGCGAACCTGACATGTGCGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
GAGAGCACCTTAACCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCCGAGCCAGGCC
CTGCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCTGTGCCAGGCCACAGCCCAGCCTCCTGTACAGGCTACAGG
TGGGCAAAGGGGGCTCTCCGGTGTCTGGGGCCCCGCGGGCCAAGGTTAGAGGTCTGGGAGAGCGCTCGTTCCCTG
ACTGAGCCCGTGTCTGCGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCCGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTTCAGCTGCGCCTGG
CGCGGAACCCGCTTCCACGGGTAACCTGGACCCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCGAGGCGACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCCTGCCG
GGCGGCGCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCCCTTC
CTGAGGGGGCCCTGTCTGCCTCCAGTGTCTGTTTTGCGCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTTGAGGCGGGGTGCGAGGGCCGTTCTGGTGGAGACATTCCCTGCCCCAGAGAGCCGCGGGGGA
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCCGTAGAGACTTGCTGCCCACTGTGCGG
ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCCATTGTGCACACTGACCACAGTGAT
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCAACCAACGGTTACTACAAGGTCCGAGGAGTCACT
GTGAGCCTGAGCCTTGCGGAAGCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCCAGGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGTTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTACCCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
CCCCGGGACTCCCCCTTCCCATATGCTGCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCACGTGTGACAT
CTTTCCAATGGAAGAGTCTCTGGGATCTCCAACCTTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCCTCCAAACTGAACACAAGGGGAGGGAAAGATCATTACATTTGTCAAGGAGCATTGTATA
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCCACCCTGGCTCTCCCTGAGGGGAACTTTGCTCGGCCAAT
GGAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCAAAATGGCCACCATCTTGATTTTACTTTCCTTAAA
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAATATTGGGATAA
AAATATTTATGTTTAATAATAAAAAAAGTCAAAGAGAAAAAAA

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FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHLHIRPVELEDEASYECQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLPFFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCVSNVAVGSA
NRSTALDVLFGPILQAKPEPVSDVGEDASFSCAWRGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEARLTVNAPPVVVALHSAPAFIRGPARLQCL
VFASPAPDAVWVSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKAS
ASFSEQNLMRIPGSSDGSRRGPEEEETGSREDRGPIVHTDHSDLVLEEGTLETKDPT
NGYYKVRGVSLSLGEAPGGGLFLPPSPPLGPPGTPTFYDFNPHLGMVPPCRLYRARG
YLTPHPRAFTSYIKPTSFPPDLAPGTPPPFYAAFTPSHPRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

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FIGURE 585

GCCCCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG
CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCAGAGAGCCGCCAAGGAAGAGAAA
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCTTCTGCTGCGCTAAGGAATGAAACCCCTTCCA
GCTCGATCTGCTCTTCGTCTGCTTCTTCTTCTCAGTCAAGAGCTGGGCCCTCCAGAAGAGAGG
ATGCTGTCTGGTGTGCGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCTTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTGAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCCTGGTGCCGCCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGGACCCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
CTACTCCAAGACCCGTCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTCGTGCCACCAACAAAGCCATCCCCGG
AGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACCTTTCCACTGCTCTGCAAAGGCCAACCCAGC
TGTCACCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCCTG
ACCCTCAAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCTTGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAACTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCGTCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCCCTTCCAGAGAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCC**TAA**CAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAACTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
AAGAGCTGTTAGTCTAGAGAGACCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAAACTTAA

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FIGURE 586

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFLLFSQELGLQKRGCCLVLGMAKDKFRRMNEGQVYSFSQQPQDQVTV
SGQPVTLTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGRKRESIVSTLFISPGDVENGQSIVCRATNKAI PGGKET
SVTIDIQHPPLVNLSEVPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVTNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVLSNEKTLTLKSVRQEDAGKYVCRAVVPVVGAGEREVTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLESSTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKGAGLEAESVPMMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRASKQECNEQGS

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTTGTTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAGAAGCATCAGAAAGCACAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTGAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCTACT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTCATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

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FIGURE 588

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEESESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLSMSWLVCCKSL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

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FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCGCTTTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCCGAAGCA
GAGCCATGAGAACCCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTA CTCTGCTCCGCCGGCCGTTT
CGCCAAGTCCTGGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCCTGCAGCAGACACACTGA
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLslGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRMDTVTMKALALLADLHPSVRQRCLIQKRRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAGMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

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FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATACCAAAGAAGAGCTACAAGTTC AACAGATGAGACGGATTTTGTTTGTGTTTGAT
GGAGGAAGAGATGATTTTTCATAATTATAATGTAGAAGAAGCTTTTAGGGTTTTTGGAACGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAAGCTTTACAGGATATGGAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAAACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAGAAATGACTCTA
GACTTGAAAACCAATTTGGCTCAACAGCTGATGCACCTTGATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTCAAGCTAAGTGTGCCCCCTGGCATCAAAAATGATGATAAAAT
ATACTAACAACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAGATGATGATGATGCATTAGTC
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTCAAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAACAGAGCCCATAAACTATGACCTCTGAGG
TTTCATTGGAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTTCATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAAGGTTTGTTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTCCCTAAATAAAAATCACCTTTTAAGCTAGAG
CGTCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTGTAGTACACCAGCTGAATACGGAGCAATGGTGTGTTAT
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

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FIGURE 592

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157.  
><subunit 1 of 1, 499 aa, 1 stop  
><MW: 56471, pI: 4.31, NX(S/T): 2  
MAAAPGLLVWLLVLRLLPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC  
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDETD  
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP  
VEANSEESDSVFSENTEDLQEQFTTQKHHSHANSQANHAQGEQASFESFEEMLQDKLKVP  
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTGFGSTADALVSDDETTRLVTSLED  
DFDEELDTTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE  
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP  
DSKQGKPQSATDYSDDPDNVDDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD  
ETELEDENQEGFKTEPIKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

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FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG
TCATGCTGCTCTGGGTCTGGTAACTCTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCTACTTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGTACGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG
GCGAATTCTGCA

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FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLNRKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

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FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAAACCAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCACGGAATTAAATTCAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCCTTCACT
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCOAAGGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579.  
><subunit 1 of 1, 285 aa, 1 stop  
><MW: 32368, pI: 5.32, NX(S/T): 0  
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI  
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISERDAAQKIYVEMKFTLRDCNSIPWVLGT  
CKETFNLFYMESESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE  
RKGFYLAQDQIGACIALVSVRVFYKKCPFTVRNLMFPDTIPRVDSSSLVEVRGSCVKSA  
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHGASKGRCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

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FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGG
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTT
GCTGTCTTGGCACTGGGCCGAAGCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCTGCTCCGGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCGCTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCAGGTACGAGAAGGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCCCAAAACCCCGGTGGCACAAAAA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTCAGGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGCGGCCGCCAGGGGCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGGCCCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTGCTGAACCTGAGCGCGCAGGGGCCCCGTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCCGGGGCGCACGGCCCGCACGACGCCTTCCG
CGCCTCGCTCAGCTGCGTGCTGCCCCGACTTCTTGCAAGGGCCGGGCGCCCGGACGTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCCCGT
CTTCACACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVNLVSEEQHFGLSLYWNQVQGPCKPRWH
KNLTGPIITLNTDILVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPLNLCV
QVNSSEKLQLOECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRLLLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFTLPSQLPDLGLG
ALQQPRAPRSGRLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

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FIGURE 599

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCAACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAGAATTTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
YDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTCTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCCCTTGACA
GTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACCTCTGAACTGTTCCATATTATAA
TAGATGTCAACAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCATCTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

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FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCIVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 604

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 605

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATGG
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTAGAAGA
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTAAAGAGCT
GGTGTGTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI

HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावDNDsfyv

EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCCATGTGGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACCTCTCCG
AACCTCTGACTAAAGACATGGCCACTTAGAGAGATGGATCTGCAGAGCCTTCCTGCCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGACT
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCGGCCCGGTGCTTGTCTCCCCCTCCCACCTCTTCTCTCCTAGCT
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACGTCTCTAGGGAAGTGGTTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCACAAAGCAAACACACCACACATGTTCCGC
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGTCTTCTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTCGAGCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TGGAATGCTTTCTTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTCAACGTGATGTCATTCTTTTCCCACCGTTTCTTCTGTTGATATTCAATGAATC
CGTCAATCTCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 608

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETIYIKWWCRGVRWDTCKI
LIETRGEQGEKSDRVSIDKNQKDRFTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNYMLLVFVKVPILLILVTAILWLKGSQRPVE
EPGEQPIYMNFEPLTKDMAT

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

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FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATAAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAATAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSLTIKKDLRLSHAMTCHCGEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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- (21) International Application Number: PCT/US01/06520
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| 60/186,968 | 6 March 2000 (06.03.2000) | US |
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| 60/189,320 | 14 March 2000 (14.03.2000) | US |
| PCT/US00/06884 | 15 March 2000 (15.03.2000) | US |
| 60/191,048 | 21 March 2000 (21.03.2000) | US |
| 60/190,828 | 21 March 2000 (21.03.2000) | US |
| 60/191,314 | 21 March 2000 (21.03.2000) | US |
| 60/191,007 | 21 March 2000 (21.03.2000) | US |
| 60/192,655 | 28 March 2000 (28.03.2000) | US |
| 60/193,032 | 29 March 2000 (29.03.2000) | US |
| 60/193,053 | 29 March 2000 (29.03.2000) | US |
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| 60/196,187 | 11 April 2000 (11.04.2000) | US |
| 60/196,690 | 11 April 2000 (11.04.2000) | US |
| 60/198,121 | 18 April 2000 (18.04.2000) | US |
| 60/198,585 | 18 April 2000 (18.04.2000) | US |
| 60/199,654 | 25 April 2000 (25.04.2000) | US |
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| PCT/US00/14042 | 22 May 2000 (22.05.2000) | US |
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| PCT/US00/15264 | 2 June 2000 (02.06.2000) | US |
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| PCT/US00/20710 | 28 July 2000 (28.07.2000) | US |
| 09/644,848 | 22 August 2000 (22.08.2000) | US |
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1 December 2000 (01.12.2000) US
PCT/US00/34956
20 December 2000 (20.12.2000) US
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- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **BAKER, Kevin, P.** [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). **CHEN, Jian** [US/US]; 121 York Drive, Princeton, NJ 08540 (US). **DESNOYERS, Luc** [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). **GODDARD, Audrey** [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). **GODOWSKI, Paul, J.** [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). **GURNEY, Austin, L.** [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). **PAN, James** [CA/US]; 2705 Coronet Boulevard, Belmont, CA 94002 (US). **SMITH, Victoria** [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). **WATANABE, Colin, K.** [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). **WOOD, William, I.** [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US). **ZHANG, Zemin** [CN/US]; 876 Taurus Drive, Foster City, CA 94404 (US).
- (74) Agents: **BARNES, Elizabeth, M.** et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.



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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER

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G01N33/53 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 63088 A (BAKER KEVIN ;CHEN JIAN (US); GENENTECH INC (US); YUAN JEAN (US); G) 9 December 1999 (1999-12-09) page 1 -page 2; claims 1-26; figures 3,4; examples 1-3,5,139-147 page 281 -page 284 page 305 -page 314 page 345 -page 373 ---	1-24
X	WO 99 54461 A (SCHMITT ARMIN ;SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND) 28 October 1999 (1999-10-28) page 1 -page 7; claims 1-38; figures 1-5; examples 1-4 see SEQ ID NO: 53 (pp.215 and 216), SEQ ID NO: 300 (pp. 350 and 351) page 163 --- -/--	1-24

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

06.06.2002

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Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

INTERNATIONAL SEARCH REPORT

Internatic..... Application No

PCT/US 01/06520

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X, L	WO 00 73454 A (GENENTECH INC) 7 December 2000 (2000-12-07) page 1 -page 2; claims 1-118; figures 3,4; examples 1-3,5,139-172 page 43 -page 44 page 283 -page 288 page 304 -page 316 page 338 page 371 -page 398 ---	1-24
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E	WO 01 57190 A (CAO YICHENG ;CHEN RUI HONG (US); GOODRICH RYLE (US); HYSEQ INC (US) 9 August 2001 (2001-08-09) page 1 -page 97; claims 1-28; examples 1-9 -& DATABASE EM GSN [Online] EBI, Hinxton, UK; AC/ID AAK52618, "SEQ ID NO: 2147" XP002191775 abstract -& DATABASE EM GSP [Online] EBI, Hinxton, UK; AC/ID AAM78501, "SEQ ID NO: 1163" XP002191776 abstract -----	1-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/06520

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 20 and 21 are directed to a method of treatment of the human/animal body (in so far as in vivo methods are concerned), the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-24 partially

* An isolated nucleic acid SEQ ID NO: 1 which encodes amino acid sequence SEQ ID NO: 2. A vector, a host cell, a process for producing a polypeptide, an isolated polypeptide encoded by said nucleic acid. A chimeric molecule, an antibody, methods for stimulating the release of TNF-alpha, for stimulating the proliferation or differentiation, for detecting the presence of tumor, an oligonucleotide probe.

Inventions 2-305: claims 1-24 partially

same as invention 1 but comprising the polynucleotide and amino acid sequence in the order given in claims 1 and 2 (invention 2 is limited to SEQ ID NO: 3 and 4 and invention 305 is limited to SEQ ID NO: 609 and 610).

INTERNATIONAL SEARCH REPORT

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